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GenCore version 5.1.6

Run on: December 12, 2005, 08:17:24 ; Search time 189 Seconds (without alignments)

Sequence: 1 MGSTSETKMSPEAAABEE.....PRVVASCAVNTWIEFLKKI 368

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 2443163 seqB, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_21:*

1: geneseqp19980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1915	100.0	368	2	AAV23342	AAV23342 A bifunct
2	1915	100.0	368	3	RAH1995	RAH1995 Sweetgum
3	1915	100.0	368	4	AAE05829	AAE05829 L. Styrac
4	1915	100.0	368	9	ADZ14866	Ad214866 Syringyl
5	195.5	83.3	365	2	AAV01133	AAV01133 Aspen bib
6	195.5	83.3	365	5	AAU80015	AAU80015 5-hydroxy
7	195.5	83.3	365	7	ADD93900	ADD93900 Quaking a
8	189.9	83.0	365	0	AAO30114	AAO30114 Strawberr
9	198.5	83.0	365	2	AAW4132	AAW4132 Embry
10	157.5	82.4	364	2	AAK34762	Aak34762 PLC4 tra
11	166.5	81.9	365	5	AAE16510	Aae16510 Soypean C
12	156.5	81.8	365	7	AD29674	Ad29674 Soypean C
13	156.5	81.8	365	8	AD29684	Ad29684 Soypean C
14	154.5	80.7	365	2	AAE6303	AAE6303 Alfalfa C
15	154.5	80.7	365	4	AAE12021	Aae12021 Medicago
16	154.5	80.7	365	8	ADK39712	Adk39712 Alfalfa C
17	152.8	79.8	370	8	ADK39713	Adk39713 Fairy fan
18	149.3	78.0	364	2	AAK34764	Aak34764 Omritran
19	149.2	77.9	358	5	AAE16517	Aae16517 Soypean C
20	149.2	77.9	358	7	AD29688	Ad29688 Soypean C
21	149.2	77.9	358	8	AD296498	Ad296498 Soypean C
22	147.3	76.9	363	3	AAE47426	Aae47426 Arabidops
23	147.3	76.9	363	5	AAE25596	Aae25596 Arabidops
24	147.3	76.9	363	5	AAE93811	Aae93811 Herbicida

Adn73	e	cr	idop	idop
Aag97	Aag97	idop	idop	idop
Aag25	Aag25	idop	idop	idop
Ady07	Ady07	t	t	t
Adk39	Adk39	frag	frag	frag
Aar34	Aar34	idop	idop	idop
Aag25	Aag25	idop	idop	idop
Aag97	Aag97	idop	idop	idop
Aaw84	Aaw84	idop	idop	idop
Aae29	Aae29	kia	idop	idop
Yfa	Yfa	Yfa	Yfa	Yfa
Aae16	Aae16	t	t	t
Adi29	Adi29	t	t	t
Adj95	Adj95	t	t	t
Adw80	Adw80	t	t	t
Abb78	Abb78	ran	ran	ran
Adf89	Adf89	um	um	um
Aar28	Aar28	in	in	in
Aab18	Aab18	in	in	in
Aae15	Aae15	in	in	in
Adi29	Adi29	in	in	in
Adj96	Adj96	in	in	in
Adw80	Adw80	in	in	in
Abb78	Abb78	in	in	in
Aab28	Aab28	in	in	in
Aab91	Aab91	in	in	in
Aae16	Aae16	in	in	in
Adi29	Adi29	in	in	in
Adj95	Adj95	in	in	in
Adl14	Adl14	in	in	in
Adk39	Adk39	in	in	in
Aab91	Aab91	in	in	in
Aag17	Aag17	idop	idop	idop
Aab91	Aab91	idop	idop	idop
Adn74	Adn74	idop	idop	idop
Aab26	Aab26	idop	idop	idop
Aag11	Aag11	idop	idop	idop
Aag11	Aag11	idop	idop	idop

98	794.5	41.5	373	5	ABB91081	Abb91081 Herbicida
99	794.5	41.5	373	8	ADN74367	Adn74367 Thale cre
100	790.5	41.3	373	5	ABB91083	Abb91083 Herbicida
ALIGNMENTS						
RESULT 1						
AAV23342						
ID	AAV23342	Standard; protein; 368 AA.				
XX						
AAV23342;						
XX						
DT	01-SEP-1999	(first entry)				
DE	A bifunctional-O-methyl transferase involved in lignin production.					
XX						
KW	Bifunctional-O-methyl transferase; syringyl lignin; angiosperm; lobolly pine; <i>Pinus taeda</i> ; lignin; woody plant; paper manufacture; delignification; pulp mill; gymnosperm.					
XX						
OS	Liquidambar styraciflua.					
XX						
XX	W0931243-A1.					
PD	24-JUN-1999.					
XX						
PP	16-DEC-1998;	98WO-US026784.				
XX						
PR	16-DEC-1997;	97US-00991677.				
XX						
PA	(INTO) INT PAPER CO.					
XX						
PT	Chiang VL,	Carraway DT,	Smeltzer RH;			
XX						
WPI:	1999-405034/34.					
XX						
DR	N-PSDB; AAX81875.					
XX						
PA	(INTO) INT PAPER CO.					
XX						
PT	Chiang VL,	Carraway DT;				
XX						
PR	26-MAR-1999;	99US-00277248.				
XX						
PA	(INTO) INT PAPER CO.					
XX						
PT	Chiang VL,	Carraway DT;				
XX						
DR	N-PSDB; AAX88683.					
XX						
PT	Use of angiosperm coniferyl aldehyde 5-hydroxylase which can be used to produce syringyl lignin in gymnosperms, especially the loblolly pine (<i>Pinus taeda</i>). It is necessary to remove much of the lignin from the fiber/lignin network of woody plants in paper manufacture.					
XX						
CC	Greater proportions of syringyl lignin result in a higher delignification rate and hence a more efficient pulp mill operation					
CC						
XX	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 2; Length 368;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0; Gaps 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence represents a bifunctional-O-methyl transferase which is involved in syringyl lignin production in an angiosperm. The sequences are used to produce syringyl lignin in gymnosperms, especially the loblolly pine (<i>Pinus taeda</i>). It is necessary to remove much of the lignin from the fiber/lignin network of woody plants in paper manufacture.					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as sweetgum that are involved in production of lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis in gymnosperm lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						
CC	expression of the introduced angiosperm DNA, which is preferentially expressed in coniferyl aldehyde 5-hydroxylase DNA (see AAX88682), is mediating the production of syringyl lignin biosynthesis					
CC						
CC	Sequence 368 AA;					
CC						
CC	Query Match 100 %; Score 1915; DB 3; Length 364;					
CC						
CC	Best Local Similarity 100.0%; Pred. No. 4.8e-196; Mismatches 368; Conservative 0; Indels 0;					
CC						
CC	Matches 368; (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	Example 1; Fig 2D-E; 83pp; English.					
CC						
CC	The present sequence is that of sweetgum bifunctional O-methyl transferase (b1-Omp), as deduced from an isolated cbn clone (see AAX88683).					
CC						
CC	enzyme is involved in the syringyl lignin biosynthetic pathway. the invention is to identify, sequence and clone specific genes involved in the production of syringyl lignin, and to then introduce such genes into the genome of angiosperm such as loblolly pine, to induce production of syringyl lignin, thereby provide enhanced pulping ability of the wood structure.					
CC						

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EE 240
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ED 238
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EC 300
|
EC 298
|
TW 360
|
TH 357

CC at least one of the specified gene (linked to a promoter and a CC terminator), a set of DNA constructs (each containing a promoter, CC and the set of above or a single construct containing the 4CL gene, where CC incorporated into a plant genome. The method is used to transform plants, CC particularly trees but also forage crops and monocots, to alter their agronomic properties, especially lignin and cellulose contents, CC byringyl/guaiacyl (S/G) lignin ratio, growth, wood quality, stress CC increase S/G ratio (this simplifies delignification in paper and pulp CC manufacture) and to increase digestibility of grasses. The present CC sequence represents quaking aspen Aldmt.

XX Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 7; length 365; Best Local Similarity 80.9%; Pred. No. 9.3e-162; Mismatches 30; Indels 3; Gaps 2; Matches 297; Conservative 80.9%; Pred. No. 9.3e-162; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSTSETKNSPSEAAAABEEAFVAMQTSASVLPVMVKAIEVDLVEITAKAGGAHTS 60
1 MGSTGETQMPHQ-VSDEBAAHLFAMQLASASVLPMLKTAIEVDLIEIMAKAGGATL 58

QY 61 TSDIASKLPTKPNPAAVMDRMLRLLASVTSVLTSLTLPDKGKVERLYGLAPVCKFLRN 120
59 TSEFAASHLPLTPKNPAPVMDRILRLLASVTSLTKDLPDKGKVERLYGLAPVCKFLRN 118

QY 121 DDGVSIAALSLMNQDKVLMESWHLTEAVLEGIPPNKAYGMTRAFYKTDPRNTVFN 180
119 EDGVSIATLCKLQMLDKVLMESWHLTEAVLEGIPPNKAYGMTRAFYKTDPRNTVFN 178

QY 181 GMSNHSTITMKKILETYKGREGISVVDVGGTGAHLNMIIAKUPMIKGINFDPHVEE 240
179 GMSNHSTITMKKILETYKGREGISLVDVGGTGAHNTVSKPSIKINFDPHVEE 238

QY 241 APSTYGVVERVGGDMFVSPKGDAITMKWICHWDNSDEHCFLKFLKCYDALPENGKVLBC 300
239 APSTYGVVERVGGDMFVSPKGDAITMKWICHWDNSDEHCFLKFLKCYDALPENGKVLBC 298

QY 301 ILPVAPDASLPTKAVHDTMLAHNPGGKERTKEFALAKGAGFEGFRWASCAVNW 360
299 ILPVAPDASLPTKAVHDTMLAHNPGGKERTKEFALAKGAGFEGFRWASCAVNW 357

QY 361 IIEFLKK 367
Db 358 VIEFRKK 364

RESULT 8

AA030114 ID AA030114 standard; protein; 365 AA.

XX AC AA030114; DT 03-SEP-2003 (first entry)

DE Strawberry O-methyltransferase (STOMT).

XX KW Strawberry; O-methyltransferase; 2,5-dimethyl-4-hydroxy-3(2H)-furanone; DT STOMT; DMHF; dithiothreitol; 2,5-dimethyl-4-methoxy-3(2H)-furanone; DTT; KW DMHF; enzyme; plant.

XX OS Fragaria x ananassa.

XX PN WO2003046163-A2.

PD 05-JUN-2003.

XX PP 26-NOV-2002; 2002WO-EP013320.

XX PR 26-NOV-2001; 2001US-0332534P.

PA (UVEA-) UNIV BAYERISCHE JULIUS MAXIMILIANS WUERZ.

XX Schwab W, Kaldenhoff R, Wein M;
PI XX WPI; 2003-522772/50.
DR XX N-PSDB; AAL60735.

PT Novel isolated strawberry O-methyltransferase polypeptide with
PT methylicating ortho-dihydroxy substituted ring system such as
PT caffeoic acid, protocatechuic aldehyde or pyrogallol.

XX PS Claim 1; Page 76-77; 78pp; English.

XX The invention relates to novel strawberry O-methyltransferase:
CC polypeptides capable of methylicating an ortho-dihydroxy sub-
CC system and nucleic acid molecules encoding such polypeptides;
CC invention is useful for methylation of an ortho-dihydroxy si-
CC ring system and/or its mimetics (such as 2,5-dimethyl-4-hy-
CC furane (DMHF) or dithiothreitol (DTR)). The invention is
CC for the synthesis of naturally occurring substances prefera-
CC ble compounds such as 2-methoxyphenol, vanillin, ferulic acid,
CC or tissue cultured cells, or to enhance the production of f-
CC ebranone (DMHF). The present sequence is *Fragaria x ananass*
CC O-methyltransferase.

XX Sequence 365 AA;

Query Match 83.0%; Score 1589.5; DB 6; length 34
Best Local Similarity 81.0%; Pred. No. 4.1e-161; Mismatches 28; Indels 3; Matches 298; Conservative 81.0%; Pred. No. 4.1e-161; Mismatches 28; Indels 3; Matches 297; Conservative 81.0%; Pred. No. 4.1e-161; Mismatches 28; Indels 3;

QY 1 MGSTSETKNSPSEAAAABEEAFVAMQTSASVLPVMVKAIEVDLVEITAKAGGAHTS 60
1 MGSTGETQMPHQ-VSDEBAAHLFAMQLASASVLPMLKTAIEVDLIEIMAKAGGATL 58

QY 61 TSDIASKLPTKPNPAAVMDRMLRLLASVTSVLTSLTLPDKGKVERLYGLAPVCKFLRN 120
59 PSDLASQPLTPKNPAPVMDRMLRLLASVTSLTCSLTLPDKGKVERLYGLAPVCKFLRN 118

QY 121 DDGVSIAALSLMNQDKVLMESWHLTEAVLEGIPPNKAYGMTRAFYKTDPRNTVFN 180
119 EDGVSIATLCKLQMLDKVLMESWHLTEAVLEGIPPNKAYGMTRAFYKTDPRNTVFN 178

QY 181 GMSNHSTITMKKILETYKGREGISVVDVGGTGAHLNMIIAKUPMIKGINFDPHVEE 240
179 GMSNHSTITMKKILETYKGREGISLVDVGGTGAHNTVSKPSIKINFDPHVEE 238

QY 241 APSTYGVVERVGGDMFVSPKGDAITMKWICHWDNSDEHCFLKFLKCYDALPENGKVLBC 300
239 APSTYGVVERVGGDMFVSPKGDAITMKWICHWDNSDEHCFLKFLKCYDALPENGKVLBC 298

QY 301 ILPVAPDASLPTKAVHDTMLAHNPGGKERTKEFALAKGAGFEGFRWASCAVNW 360
299 ILPVAPDASLPTKAVHDTMLAHNPGGKERTKEFALAKGAGFEGFRWASCAVNW 357

QY 361 IIEFLKK 367
Db 358 VIEFRKK 364

RESULT 9

AAW4132 ID AAW4132 standard; protein; 365 AA.

XX AC AAW4132; DT 11-FEB-1999 (first entry)

DE Exemplary caffeoic acid methyl transferase COMT sequence.

XX KW (iso) eugenol methyl transferase; IEMT; lignin reduction; KW phenylpropanoid biosynthetic pathway; methyl-isoeugenol;

Db 239 APSPGVEHGGDMFVSPCADAVFMKWHIDWSDAHCFLKNCYDALPENGKVLVFC 298
 QY 301 ILPAPDASLPTKAVHIDVMLAHNPGGKERTKEFEALAKGAGFEGFRVWASCAVNW 360
 Db 299 ILPAPDASLPTKAVHIDVMLAHNPGGKERTKEFEALAKGAGFEGFRVWMC-CAFNTH 357
 QY 361 IIEFLK 366
 :|:
 Db 358 VIEFLK 363

RESULT 11
 AAEI6510
 ID AAEI6510 standard; protein; 365 AA.
 XX
 AC AAEI6510;
 XX
 DT 09-APR-2002 (first entry)
 DE Soybean caffeic acid 3-O-methyltransferase (COMT) #1.
 XX
 KW Soybean; caffeic acid 3-O-methyltransferase; COMT; caffeic acid;
 KW 5-hydroxyferulic acid O-methyltransferase; phenylpropanoid;
 KW transgenic plant; 5-hydroxyferulic acid; injury-repair mechanism;
 KW papermaking; host defect repair mechanism; lignin biosynthesis;
 OS Glycine max.
 XX
 PN US7329204-B1.
 XX
 PD 11-DEC-2001.
 XX
 PF 09-FEB-2000; 2000US-00500569.
 XX
 PR 10-FEB-1999; 99US-0119587P.
 XX
 (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PA Cahoon RE, Rafalski JA, Shen JB;
 XX
 PT WPI; 2002-121138/16.
 DR N-PSDB; ADI29674.
 XX
 PT New polynucleotide encoding caffeic acid 3-O-methyltransferase from rice,
 PT used for studying lignin biosynthesis and in positive selection
 PT systems.
 XX
 PS Example 3; Page 27-30; 34pp; English.

The invention relates to an isolated nucleic acid fragment encoding
 CC caffeic acid 3-O-methyltransferase (COMT) (also known as caffeic acid/5-
 CC hydroxyferulic acid O-methyl transferase) involved in phenylpropanoid
 CC metabolism. COMT is involved in the biosynthesis of the mono- or
 CC dimethoxylated lignin precursors. COMT DNA is used to produce transgenic
 CC plants or microbes that have altered levels of methylation for both
 CC caffeic and 5-hydroxyferulic acids, so can provide a method for positive
 CC selection. Since caffeic acid 3-O-methyltransferase is involved in lignin
 CC biosynthesis, the transgenic plants may have altered contents, or types,
 CC of lignin, so may be better suited for papermaking, and COMT DNA can also
 CC be used to study synthesis of lignin in plant cells, including its role
 CC in host defect- and injury-repair mechanisms. The present sequence is
 CC soybean COMT protein
 XX
 SQ Sequence 365 AA;

Query Match 81.8%; Score 1566.5; DB 5; Length 365;
 Best Local Similarity 80.2%; Pred. No. 1.2e-158;
 Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSTETKPSSEAAAEAAAFVAFMQLTSAVLPVNLQSAEVDLVEIMAKGAGHMS 60
 :|:
 1 MGSGTETQITPTH--VSDEPANLFLAMQLASVPLMILKSAEEDLLEIKAQPGVHLS 58

RESULT 12
 ADI29674
 ID ADI29674 standard; protein; 365 AA.
 XX
 AC ADI29674;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Soybean caffeic acid 3-O-methyltransferase homologue sequen
 XX
 KW caffeoic acid 3-O-methyltransferase; phenylpropanoid metaboli
 XX
 OS Glycine max.
 XX
 PN US6610521-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 05-OCT-2001; 2001US-00971823.
 XX
 PR 10-FEB-1999; 99US-0119587P.
 XX
 PR 09-FEB-2000; 2000US-00500569.
 XX
 (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 DR N-PSDB; ADI29673.
 XX
 PT Cahoon RE;
 XX
 PT WPI; 2003-895338/82.
 XX
 PT New polynucleotide having a sequence encoding a polypeptide
 PT caffeic acid 3-O-methyltransferase activity, useful for pro
 PT level of the protein involved in phenylpropanoid metabolis
 PT transformed host cell.
 XX
 PS Claim 4; SEQ ID NO 4; 35pp; English.
 XX
 CC This invention relates to a novel isolated polynucleotide wi
 CC a nucleotide sequence or its complement encoding a polypepti
 CC activity of caffeic acid 3-O-methyltransferase. The amino ac
 CC of the polypeptide has at least 92% identity with the fully
 CC amino acid sequence based on the clustal alignment method.
 CC polynucleotide is useful for producing altered levels of th
 CC involved in phenylpropanoid metabolism in a transformed host
 XX
 SQ Sequence 365 AA;

QY 61 TSDIASKUPKPNPDAVMDRMRLASYSVUTCSLRITPDGKTRLYGL
 :|:
 59 PTDISQSLTQNPDAPVMDRILRLACNMLPSRLTLPDKYERLGL
 DB 121 DDGYSIAALSLIMNQDKVLMESWMLTEAVTEGGIPFPNKAYGMATPEYGT
 QY 119 EDGVSTAAALMNLQDKVLMESWYIKDAVLEGGIPFPNKAYGMATPEYGT
 181 GMSHSHSTIMKKLILETYKCEFGEGLSWVGGGCAHLLNNIAKYPMIGI
 DB 179 GMADHSTITMKKILETYKCEFGESLKLSDVGGGTGAVINMVKHPTKGI
 QY 241 APSPGVEHGGDMFVSPKGDAIFMKWICHDMDSBHCFLKFLKCYEALP
 DB 239 APSPGVEHGGDMFASVKAFLFMKWHIDWSDHCLKFLKNCYEAFLP
 QY 301 ILPAPDASLPTKAVHIDVMLAHNPGGKERTKEFEALAKGAGFEGFR
 DB 299 ILPAPDSSALPTKAVHIDVMLAHNPGKERTKEFEALAKGAGFEGFR
 QY 361 IIEFLKKI 368
 :|:
 DB 358 IMEFLKKI 365

IN 120
 :|:
 QN 118
 IN 180
 :|:
 VR 178
 :|:
 JE 240
 :|:
 JD 238
 :|:
 3C 300
 :|:
 3C 298
 :|:
 TW 360
 :|:
 IN 357

XX
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
XX
PT DIXON RA, NI W;
XX
DR WPI; 1994-33204/41.
XX
DR N-PSDB; AAQ77692.
PT Reducing lignin content in plants - by transfection with an anti-sense
gene for caffeic acid 3-O-methyl-transferase gene.
XX
PS Disclosure; Page 21-23; 39pp; English.
XX
CC Alfalfa cOMT clone pCOMT1, obtained from a cDNA library in lambda ZAP II.
was the basis of antisense genes used to reduce the lignin content of
e.g. tobacco and alfalfa. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 365 AA;
Query Match 80.7%; Score 1544.5; DB 2; Length 365;
Best Local Similarity 78.8%; Pred. No. 2.8e-156; Indels 3; Gaps 2;
Matches 290; Conservative 42; Mismatches 33; Del 1;
1 MGSETSETKNSPSEAAAEBAFVAFAMQTSASVLPVNUKSAIEDVLEIMAKQGAMTS 60
1 MGSGTGETOITPTH--ISDEBANFAMQLASAVLPVNUKSAILEDVLEIMAKQGAGTS 58
61 TSDIASKUPLTKPNPDAVMDRMLRMLLASYSVLTSLSRLTPDGKTERLYQKLPVCKLTM 120
59 PIETASQQLPTNPDAVMDRMLRMLLACYVILTSLSRLTPDGKTERLYQKLPVCKLTM 118
121 DDGVISIAALSLMNOQDKVLMESWVHILTEAVLEGGLGPKAYGMFTAFYHGTDPREN 180
119 EDGVISIALNLMNOQDKVLMESWVHILDAVLDGGIPKNAKGMTAFYHGTDPREN 178
181 GMSHSTITMKKILETYKPEGGLGSWVHILTEAVLEGGLGPKAYGMFTAFYHGTDPREN 240
179 GMSHSTITMKKILETYTPEGGLGSWVHILDAVLDGGIPKNAKGMTAFYHGTDPREN 238
241 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 300
239 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 298
301 ILPVAPDASLPTKAVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVVASCAVNTW 360
299 ILPVAPDSSLATKGVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVHN-AFTNTY 357
361 IIEFLKKI 368
358 IIEFLKKV 365
RESULT 15
AAB12021 ID AAB12021 Standard; protein; 365 AA.
AC AAB12021;
XX
DT 18-DEC-2001 (first entry)
XX
DE Medicago sativa caffeoyl CoA 3-O-methyltransferase (cCOMT) protein.
XX
KW Alfalfa; caffeoyl CoA 3-O-methyltransferase; cCOMT; lignin; woody plant;
KW forage legume; transgenic plant; paper industry.
XX
OS Medicago sativa.
XX
WO2001/3090-A2.
XX
PD 04-OCT-2001.
XX
PP 23-MAR-2001; 2001WO-US009398.
XX
PR 24-MAR-2000; 2000US-0192086P.
XX
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
XX
PT DIXON RA, GUO D;
XX
DR WPI; 2001-616527/71.
XX
DR N-PSDB; AAD19546.
PT Transforming forage legumes for modifying lignin composition
PT increasing in vivo digestibility comprises transforming plant
PT lignin biosynthetic enzyme genes under lignification-associ-
specific promoter.
XX
PS Example 1; Page 52-53; 53pp; English.
XX
CC The invention relates to methods for producing forage legum-
CC plants having altered lignin composition. Methods for trans-
CC legumes with a DNA construct comprises alfalfa caffeic acid
CC methyltransferase (cCOMT), caffeoyl CoA 3-O-methyltransferase
enzyme or its fragment under a lignification-associated tis-
CC promoter, resulting in the down regulation of the correspond-
CC ing homologous cOMT genes either through antisense inhibition or
CC suppression. The methods are useful for down-regulation of
CC corresponding homologous cOMT genes, gene silencing, reduced
CC lignin content, reduced lignin composition, and modified lignin compo-
CC nition in transgenic plants, and increased digestibility of transgenic
CC materials in ruminant animals. The expression of cCOMT trans-
CC CC plant and greatly improved forage in vivo digestibility, and
CC lignins with altered dimer bonding patterns. Transforming for-
CC aging cOMT enzymes is useful to produce plants having modified
CC content and composition for direct comparison of the effect
CC content and/or composition of forage digestibility. The method
CC is useful for producing plants that are modified to alter lignin
CC sequence is alfalfa caffeoyl CoA 3-O-methyltransferase (cCOMT)
XX
SQ Sequence 365 AA;
Query Match 80.7%; Score 1544.5; DB 4; Length 365;
Best Local Similarity 78.8%; Pred. No. 2.8e-156; Indels 3; Gaps 2;
Matches 290; Conservative 42; Mismatches 33; Del 1;
1 MGSETSETKNSPSEAAAEBAFVAFAMQTSASVLPVNUKSAIEDVLEIMAKQGAMTS 60
1 MGSGTGETOITPTH--ISDEBANFAMQLASAVLPVNUKSAILEDVLEIMAKQGAGTS 58
61 TSDIASKUPLTKPNPDAVMDRMLRMLLACYVILTSLSRLTPDGKTERLYQKLPVCKLTM 120
59 PIETASQQLPTNPDAVMDRMLRMLLACYVILTSLSRLTPDGKTERLYQKLPVCKLTM 118
121 DDGVISIAALSLMNOQDKVLMESWVHILTEAVLEGGLGPKAYGMFTAFYHGTDPREN 180
119 EDGVISIALNLMNOQDKVLMESWVHILDAVLDGGIPKNAKGMTAFYHGTDPREN 178
181 GMSHSTITMKKILETYKPEGGLGSWVHILTEAVLEGGLGPKAYGMFTAFYHGTDPREN 240
179 GMSHSTITMKKILETYTPEGGLGSWVHILDAVLDGGIPKNAKGMTAFYHGTDPREN 238
241 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 300
239 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 298
301 ILPVAPDASLPTKAVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVVASCAVNTW 360
299 ILPVAPDSSLATKGVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVHN-AFTNTY 357
361 IIEFLKKI 368
358 IIEFLKKV 365
XX
PR 241 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 300
239 APSYPGVHEVGGDMEVSVPKGDAIFMKWICHDWSDEHCKLKKCYEALPTNGKVLABC 298
301 ILPVAPDASLPTKAVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVVASCAVNTW 360
299 ILPVAPDSSLATKGVWHIDVIMLAHNPQGKERTKEFEALAKGAGPEGFPRVHN-AFTNTY 357
361 IIEFLKKI 368
358 IIEFLKKV 365

#Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rag

ge 11

Search completed: December 12, 2005, 09:33:30
Job time : 194 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 12, 2005, 08:27:04 ; Search time 39 Seconds

(without alignments)
 907.892 Million cell updates/sec

Title: US-10-681-878a-6
 Perfect score: 1915
 Sequence: 1 MGSTSETKMSPEAAABEE.....FRVWASCAYNTWIEFLKKI 368

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : PIR_80,*
 1: pir1,*
 2: pir2,*
 3: pir3,*
 4: pir4,*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1595.5	83.3	365	2 S18569	lignin-bispecific
2	1544.5	80.7	365	2 T09673	cafeate O-methyl
3	1535.0	80.2	366	2 S40146	catechol O-methyl
4	1527.5	79.8	359	2 T12259	O-diphenol O-methyl
5	1510.0	78.9	364	2 T09780	probable caffeate
6	1499.5	78.3	364	2 S36403	catechol O-methyl
7	1494.5	77.5	364	2 T12260	catechol O-methyl
8	1403.5	73.3	350	2 T12260	caffeyl-CoA O-met
9	1185.0	61.9	364	2 S28612	catechol O-methyl
10	1052.5	55.5	365	2 T02344	catechol O-methyl
11	1047.0	54.7	365	2 S22696	myo-inositol O-met
12	836.0	43.7	372	2 T09617	isoliquiritigenin
13	832.0	43.4	363	2 E9559	hypothetical prote
14	831.5	43.4	381	2 G96804	hypothetical prote
15	830.5	43.4	381	2 F96804	hypothetical prote
16	811.5	42.4	352	2 H96556	CDS Protein_Full
17	803.5	42.0	373	2 E86344	hypothetical prote
18	794.5	41.5	373	2 B86344	hypothetical prote
19	790.5	41.3	373	2 D86344	probable O-methyl
20	789.5	41.2	373	2 C86344	hypothetical prote
21	780.5	40.8	381	2 H96556	hypothetical prote
22	736.5	38.5	367	2 E96795	hypothetical prote
23	711.0	37.1	382	2 T09600	catechol O-methyl
24	686.5	35.8	376	2 T06189	probable catechol
25	596.0	31.1	359	2 T46100	cafeic acid O-met
26	510.0	26.6	205	2 E96653	hypothetical prote
27	456.0	23.8	382	2 T04963	catechol O-methyl
28	402.0	21.0	352	2 T09707	isoflavanone-O-methyl
29	396.5	20.7	325	2 T04962	catechol O-methyl

ALIGNMENTS

line: caffeic acid
ID:9166419; PID:
3 2;
3 60
3 58
DN 120
DN 118
MN 180
JK 178
SE 240
3D 238
3C 300
3C 298
TW 360
NY 357
3 3;
4T 59
3L 58

Qy 60 STDIAISKLPTKPNPDAVMILRMLLASVTSIRTLPDGKIERLYGLAPVCKFLTR 119
 Db 59 SPGEVARQLPQTNPAPVMLDRIFRLIASVLTCTLNLPDGKVERLYGLAPVCKFLV 118

Qy 120 NDDGSIASLMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 179
 Db 119 NEDGVSIASLMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 179
 C;Species: Capsicum annuum (pepper)
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000

Qy 180 NGMSNISTITMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 239
 Db 179 RGMSPHSITMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 239
 C;Accession: T12259
 R;Hu, W.J.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z1649
 A;Accession: T09780
 A;Species: Populus tremuloides (quaking aspen)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 004

Qy 240 EAPSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 299
 Db 239 DAPPLPGVKHVGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 299
 C;Accession: T09780
 R;Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 300 CILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 359
 Db 299 CILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 359
 C;Accession: T1364
 A;Residues: 1-364 <HNU>
 A;Cross-references: UNIPROT:Q41086; UNIPARC:UPI000009D55C; EMBL: NID:91236979; PIR: 357

Qy 360 WIEFK 366
 Db 358 HMEFK 364

RESULT 4

T12259 O-diphenol-O-methyltransferase (EC 2.1.1.-) - pepper

C;Species: Capsicum annuum (pepper)
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

A;Title: Isolation and characterization of o-diphenol-O-methyltransferase cDNA Clone in A;reference number: Z17476
 A;Accession: T12259
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-359 <LEB>
 A;Cross-references: UNIPARC:UPI00000ABB7A; EMBL:U83789; NID:91791351; PID:91791352
 A;Experimental source: very young green fruit
 C;Superfamily: O-methyltransferase
 C;Keywords: O-methyltransferase

Query Match 79, 8%; Score 1527.5; DB 2; Length 359; Best local Similarity 77.9%; Pred. No. 2.7e-116; Matches 285; Conservative 35; Mismatches 39; Indels 7; Gaps 2; Matches 285; Conservative 35; Mismatches 39; Indels 7; Gaps 2;

Qy 1 MGSTSBTKSPSEAAAEEERAVFVAMQTSASVPLVNLKSAEIDVLEM 181
 Db 1 MGSTSBTKSP- -AQIIDEA-NFALQISSLSSVPLVNLKTAEIDLEIM 181
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 61 TSDIASKLPTKPNPDAVMILRMLLASVTSIRTLPDGKIERLYGL 58
 Db 58 PSDIASHLPTKPNPDAVMILRMLLASVTSIRTLPDGKIERLYGL 58
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 121 DDGSIASLMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 118
 Db 118 EDGVSVSPLQMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 118
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 181 GMSNISTITMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 178
 Db 178 GMSTBTKMAMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 178
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 241 APSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 238
 Db 238 APAPFGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 238
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 301 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 298
 Db 298 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 298
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 361 WIEFK 367
 Db 357 VIEFK 363

RESULT 5

S3603 catchol O-methyltransferase (EC 2.1.1.6) - common tobacco

C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 004

Qy 241 APSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 300
 Db 235 APAPFGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 294
 C;Accession: S36403
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 301 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 360
 Db 295 ILPAPDTSKATKVNHWVIMLAHNPGKERTKEPEALAKAGFEGFR-RACAYQTW 353
 C;Accession: S36403
 A;Residues: 1-364 <LEB>
 A;Cross-references: UNIPROT:Q42958; UNIPARC:UPI000002D50B; EMBL: NID:9396588; PID: 353

Qy 361 IIEFK 366
 Db 354 VMEFH 359

RESULT 5

T09780 probable caffate O-methyltransferase (EC 2.1.1.6) G2 - quaking aspen

C;Species: Populus tremuloides (quaking aspen)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 004

Qy 240 EAPSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 299
 Db 239 DAPPLPGVKHVGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 299
 C;Accession: T09780
 R;Hu, W.J.
 submitted to the EMBL Data Library, March 1996
 A;Reference number: Z1649
 A;Accession: T09780
 A;Species: translated from GB/EMBL/DDJB

A;Molecule type: DNA
 A;Residues: 1-364 <HNU>
 A;Cross-references: UNIPROT:Q41086; UNIPARC:UPI000009D55C; EMBL: NID:91236979; PIR: 357

A;Experimental source: strain Mcb8
 C;Genetics:
 A;Gene: OMFG2
 A;Introns: 139/2; 243/1; 264/3
 C;Superfamily: O-methyltransferase
 C;Keywords: lignin biosynthesis; methyltransferase; S-adenosylme

Query Match 78, 9%; Score 1510; DB 2; Length 364
 Matches 285; Conservative 38; Mismatches 39; Indels 9; 3;

Qy 1 MGSTSBTKSPSEAAAEEERAVFVAMQTSASVPLVNLKSAEIDVLEM 181
 Db 1 MGSTSBTKSP- -AQIIDEA-NFALQISSLSSVPLVNLKTAEIDLEIM 181
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 61 TSDIASKLPTKPNPDAVMILRMLLASVTSIRTLPDGKIERLYGL 58
 Db 58 PSDIASHLPTKPNPDAVMILRMLLASVTSIRTLPDGKIERLYGL 58
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 121 DDGSIASLMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 118
 Db 118 EDGVSVSPLQMLNQDKVLMESWYHTEAVLEGGLPFNKAQGMTRFAYKGTPRNTVEN 118
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 181 GMSNISTITMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 178
 Db 178 GMSTBTKMAMKKILETYKGSEGGLGSVVDVGGTGAHLNMIAKCPMKGTFAYKGTPRNTVEN 178
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 241 APSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 238
 Db 238 APAPFGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 238
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 301 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 298
 Db 298 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 298
 C;Accession: T12259
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 361 IIEFK 367
 Db 357 VIEFK 363

RESULT 6

S3603 catchol O-methyltransferase (EC 2.1.1.6) - common tobacco

C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 004

Qy 241 APSYGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 300
 Db 235 APAPFGVERVGGDMFVSPKGDAIFMKWICHWDSEDEHCKFLKLYCEALPNTNGKVLAB 294
 C;Accession: S36403
 R;Lee, D.; Lee, K.W.
 J. Plant Biol. 41, 9-14, 1998

Qy 301 ILPVARDASPLTKAVHIDVIMLAHNPGKERTKEPEALAKAGFEGFRVWVACANT 360
 Db 295 ILPAPDTSKATKVNHWVIMLAHNPGKERTKEPEALAKAGFEGFR-RACAYQTW 353
 C;Accession: S36403
 A;Residues: 1-364 <LEB>
 A;Cross-references: UNIPROT:Q42958; UNIPARC:UPI000002D50B; EMBL: NID:9396588; PID: 353

C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 78.3%; Score 1499.5; DB 2; Length 364;
Best local Similarity 77.8%; Pred. No. 2e-115;
Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

Qy 1 MGSTSBTKMSPSEAAAEEAFVAFNQLTASVLPNLKSAIEJDVLEIMAKAGSGAHTS 60
1 MGSTSBSQ- SNSLITDEBAAFLFAMQLCASVLPNLKSAEVDLJELMAKAGSGAITS 58

Qy 61 TSDIASKLPTKPNPDAAVMLDMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 120
59 PSELAQQLSTONPEAPVMDLMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 118

Db 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPNPKAYGMAFEYHGDPRNTVFN 180
119 ADGVSVAPLMLNQDKVLMESWYHLDKDAVIDGGIFPNKAKGMAFEYHGDPRNTVFN 178

Qy 181 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 240
179 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 238

Db 241 APSYGVHGGDMFVSPKGDAIFKWKICHWDSDBHCFLKPKCYEALPNTGKYLASC 300
239 APTVPGVHVGDMFASVPKADAFWKWICHWDSDBHCFLKPKCYEALPANGKVIAC 298

Qy 301 ILPVARDASLPTKAVHIDVIMLAHNGGKERTEEFEALAKGCFEGF- RVVASCANT 359
299 ILPEAPDTSLATKNTVHDVIMLAHNGGKERTEEFEALAKGCFEGF- RVVASCANT 358

Qy 360 W 360
Db 359 W 359

RESULT 7

Query Match 73.3%; Score 1403.5; DB 2; Length 31;
Best local Similarity 74.6%; Pred. No. 1.5e-107;
Matches 261; Conservative 46; Mismatches 42; Indels 1;

Qy 18 EEEAFVFMQLTASVLPNLKSAIEJDVLEIMAKAGSGAHTSDIASQ 77
1 EDEACSYAMVITSGSVPVNLKAVETDLEBIIKRAKGPGQQLSPAEIANQI 77

Db 78 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 137
121 LMESYHLDKDAVLDGGLIPNPKAYGMSAFYHGDPRNTVFNMSNHSI: 137

Db 61 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 120
R;Legrand, M.
Submitted to the EMBL Data Library, August 1993

A;Reference number: S36403
A;Accession: S36404
A;Molecule type: mRNA
A;Residues: 1-364 <LEG>

A;Cross-references: UNIPROT:065362; UNIPARC:UPI00000A4A72; EMBL:36404 <LEG>

Query Match 77.5%; Score 1484.5; DB 2; Length 364;
Best Local Similarity 77.0%; Pred. No. 3.4e-114;
Matches 278; Conservative 38; Mismatches 42; Indels 3; Gaps 2;

Qy 1 MGSTETKMSPEAAAEEAFVAFNQLTASVLPNLKSAIEJDVLEIMAKAGSGAHS 60
1 MGSTSBSQ- SKSLITDEBAAFLFAMQLCASVLPNLKSAEVDLJELMAKAGSGAITS 58

Db 61 TSDIASKLPTKPNPDAAVMLDMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 120
59 PSELAQQLSTONPEAPVMDLMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 118

Db 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPNPKAYGMAFEYHGDPRNTVFN 180
119 ADGVSVAPLMLNQDKVLMESWYHLDKDAVIDGGIFPNKAKGMAFEYHGDPRNTVFN 178

Qy 181 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 240
179 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 238

Db 241 APSYGVHGGDMFVSPKGDAIFKWKICHWDSDBHCFLKPKCYEALPANGKVIAC 300
153 APSYGVHVGDMFVSPKGDAIFKWKICHWDSDBHCFLKPKCYEALPANGKVIAC 300

Db 239 APAYPGVHEVGGDMFASVPKADAFMKWICHDMSDEHCLKFLKNCYEALPJ

Qy 301 ILPVARDASLPTKAVHIDVIMLAHNGGKERTEEFEALAKGCFEGF-1 3C 298
119 ILPVARDASLPTKAVHIDVIMLAHNGGKERTEEFEALAKGCFEGF-1 VT 359
Db 299 ILPERAPDTSLATKNTVHDVIMLAHNGGKERTEEFEALAKGAGFTGFAI : 358

Qy 360 W 360
Db 359 W 359

RESULT 8

Query Match 73.3%; Score 1403.5; DB 2; Length 31;
Best local Similarity 74.6%; Pred. No. 1.5e-107;
Matches 261; Conservative 46; Mismatches 42; Indels 1;

Qy 18 EEEAFVFMQLTASVLPNLKSAIEJDVLEIMAKAGSGAHTSDIASQ 77
1 EDEACSYAMVITSGSVPVNLKAVETDLEBIIKRAKGPGQQLSPAEIANQI 77

Db 78 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 197
121 LMESYHLDKDAVLDGGLIPNPKAYGMSAFYHGDPRNTVFNMSNHSI: 197

Db 61 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 180
R;Legrand, M.
Submitted to the EMBL Data Library, August 1993

A;Reference number: S36403
A;Accession: S36404
A;Molecule type: mRNA
A;Residues: 1-364 <LEG>

A;Cross-references: UNIPROT:065362; UNIPARC:UPI00000A4A72; EMBL:36404 <LEG>

Query Match 73.3%; Score 1403.5; DB 2; Length 31;
Best local Similarity 74.6%; Pred. No. 1.5e-107;
Matches 261; Conservative 46; Mismatches 42; Indels 1;

Qy 18 EEEAFVFMQLTASVLPNLKSAIEJDVLEIMAKAGSGAHTSDIASQ 77
1 EDEACSYAMVITSGSVPVNLKAVETDLEBIIKRAKGPGQQLSPAEIANQI 77

Db 78 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 137
121 LMESYHLDKDAVLDGGLIPNPKAYGMSAFYHGDPRNTVFNMSNHSI: 137

Db 61 MLDRMLLRLASYSITLCSLRTLPGKTYEGLYGLAPVKFLTRNDGVSIA 120
R;Legrand, M.
Submitted to the EMBL Data Library, August 1993

A;Reference number: S36403
A;Accession: S36404
A;Molecule type: mRNA
A;Residues: 1-364 <LEG>

A;Cross-references: UNIPROT:065362; UNIPARC:UPI00000A4A72; EMBL:36404 <LEG>

Query Match 77.5%; Score 1484.5; DB 2; Length 364;
Best Local Similarity 77.0%; Pred. No. 3.4e-114;
Matches 278; Conservative 38; Mismatches 42; Indels 3; Gaps 2;

Qy 1 MGSTETKMSPEAAAEEAFVAFNQLTASVLPNLKSAIEJDVLEIMAKAGSGAHS 60
1 MGSTSBSQ- SKSLITDEBAAFLFAMQLCASVLPNLKSAEVDLJELMAKAGSGAITS 58

Db 61 TSDIASKLPTKPNPDAAVMLDMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 120
59 PSELAQQLSTONPEAPVMDLMLRLLASYSITLCSLRTLDGKIRLYGLAPVKFLTRN 118

Db 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPNPKAYGMAFEYHGDPRNTVFN 180
119 ADGVSVAPLMLNQDKVLMESWYHLDKDAVIDGGIFPNKAKGMAFEYHGDPRNTVFN 178

Qy 181 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 240
179 GMSNISITITMKLLETYKGFBGLGSVVDGGTGAHNMIAKYMIGNFDLPHVIE 238

Db 241 APSYGVHVGDMFVSPKGDAIFKWKICHWDSDBHCFLKPKCYEALPANGKVIAC 300
241 APSYGVHVGDMFVSPKGDAIFKWKICHWDSDBHCFLKPKCYEALPANGKVIAC 300

3C 298

VT 359

358

3C 298

VT 359

from Zea mays L.

A;Cross-references: UNIPROT:Q06509; UNIPARC:UPI0000127EA6; EMBL:M73235; NID:91256711; PID:QY	Db	61 :: : : :: : : : : : : :	vr 118
C;Genetics:			
A;Introns: 141/2			
C;Superfamily: O-methyltransferase; S-adenosylmethionine			
C;Keywords: methyltransferase			
Query Match	61.9%; Score 1185; DB 2; Length 364;		
Best Local Similarity	61.8%; Pred. No. 1-49-89; Mismatches 77; Indels 14; Gaps 7;		
Matches	230; Conservative 51; Mismatches 77; Indels 14; Gaps 7;		
QY	1 MGSTSETKONPSEAAABEEAFVAFMQLTASAVLPNVLKSAEVDYDTEIMAK-MGPG-AH 58	Db	119 DEDGASMGPLIALQDQRFVINSWFLKDAVLBGGPPFDRLRVGVHAFEP
	1 MGST-----AGDVAAVDDEBACMYAMQQLASSILPMLKNAIEGLILEVQKEAGGKAA 55	Qy	120 NDDGYSIAAALSLMNQDKVLMESWHLTEAVLEGGTIPENKYGMT-AFSTYB
	59 ISTDIASKLPTKND--AAVMFLRMRLJLASSLVSULCSRLTLPDGKIERLYGLAPVCK 115	Db	179 NNGMSNHSTIMKKILETYKPEGEGSUVTDGGTGAHIMIIXYPMK
	56 LAPBEVVARMPAAASDPPAAMAMVURMLRASLKVWR-COMED-RDGRYERRVSAAPVCK 114	Qy	179 NKAMINHTTVMKKILENYKGPFENLKTLYDVGGLGVNLKMTSKPTK
QY	116 FLTRNRNDGJUSIAALSLMNQDKVLMESWHLTEAVLEGGTIPENKYGMT-AFSTYB 175	Db	199 ECLRVAPDASLPTKAVVHIDVIMLAHNPGKGERTEKEFALAKGAGFEG
	115 WLTNPEDGVSMAALALMNQDKVLMESWHLTEAVLEGGTIPENKYGMT-AFSTYB 174	Qy	239 EBARSPGCHVNGGDMFSPKPGDIAFMKICHOMSDEFLQKFLKRCBA
	176 TVERNGMSNISTIMKKILETYKGERGLSASWVPGGGTGAHNLMIAKYPMIKGINFDP 235	Db	239 QHABSPYGVHVGGMFESTPEGDAIFMKTWILHWSDSNLKLNKCYKA
	175 RVFENGMKNSVLTTRKLUDPYTSPEGVSTLUDVGGVGATLHATTSRAPHISVNFDLP 234	Qy	299 ECLRVAPDASLPTKAVVHIDVIMLAHNPGKGERTEKEFALAKGAGFEG
Db	236 HVIBEARPSVPGVETVGGDMVSVPGKDATFMKWICHDMSDHECLKFLKKCYEAALPTNGKV 295	Db	299 EALIVPKPDIDTAVVGSQCDLIMAQNPGKERSBEEFRALATEBAGKG
QY	235 HVISBAPPFFGVVRVGGDMFASVPGDAIALMKWILHDWSDAHCATLKLKCYDAPENGKV 294	Qy	359 TWIETPLK 366
Db	296 IIAECILPVADASLPTKAVVHIDVIMLAHNPGKGERTEKEFALAKGAGFEG 355	Db	358 FWWMBCK 365
QY	295 IIVCEVLPVTEATPKAQGVFHVDMIMLAHNPGKGERTEKEFALAKGAGFEGK-ATV 352	Qy	
Db	356 AY-NWIIIEFLK 366		
Db	353 IYANAWAIEFIK 364		
RESULT 10			
J02344	catechol O-methyltransferase (EC 2.1.1.6) III - common tobacco		
C;Species: Nicotiana tabacum (common tobacco)			
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004			
C;Accession: J02344; P00814			
R;Pellegrini, L.; Geoffroy, P.; Fritig, B.; Legrand, M.			
R;Plant Physiol. 103: 509-517, 1993			
A;Title: Molecular cloning and expression of a new class of ortho-diphenol-O-methyltransferase			
A;Reference number: J02344; MUID:194302149; PMID:7518088			
A;Accession: J02344			
A;Molecule type: mRNA			
A;Residues: 1-365 <PEL1>			
A;Title: Molecular cloning and expression of a new class of ortho-diphenol-O-methyltransferase			
A;Reference number: J02344; MUID:194302149; PMID:7518088			
A;Cross-references: UNIPROT:Q42949; UNIPARC:UPI00000ACDD; EMBL:X71430; NID:9429113; PID:QY			
A;Molecule type: protein			
A;Residues: 8-33,55-61,106-114,126-145,161-169,175-180,181-191,193-198,199-204,205-218,2			
A;Cross-references: UNIPARC:UPI0000178C32; UNIPARC:UPI0000178C33; UNIPARC:UPI0000178C34; UNIPARC:UPI0000178C35; UNIPARC:UPI0000178C36; UNIPARC:UPI0000178C37			
A;Experimental source: leaf, cv. Sambum NN			
C;Genetics:			
A;Gene: OMT			
C;Superfamily: O-methyltransferase; S-adenosylmethionine			
C;Keywords: methyltransferase; S-adenosylmethionine			
Query Match	55.5%; Score 1062.5; DB 2; Length 365;		
Best Local Similarity	57.6%; Pred. No. 1-66-79; Mismatches 51; Indels 11; Gaps 7;		
Matches	212; Conservative 51; Mismatches 51; Indels 11; Gaps 7;		
QY	5 SETKNSPNSAARAAEAFVAMQLTASVLPNVKSAEVDVLMIAKAGPAGHISTDI 64	Db	197 NGFDNVKVLVDVGGAGVNSMIVAKHTHKGIVNDLPHVIAAPSYCV
	3 SSTK-SOIPQSEERNCYTAMOLISSLSSVLPFVHARSTIQEVEFLAKSN-DTQKASOI 60	Db	197 NGFDNVKVLVDVGGAGVNSMIVAKHTHKGIVNDLPHVIAAPSYCV
Db	258 VPKDAAIFWKWICHDMSDHECLKFLKKCYEAALPTNGKVLAECTLPVADP	Qy	258 VPKDAAIFWKWICHDMSDHECLKFLKKCYEAALPTNGKVLAECTLPVADP
QY	65 ASKUPT-KNPKDAAMFLDRMRLLASVLTCSLRLTPD---GKIERLYGLAPVCKFLTR 119	Db	257 IPQDAIFWKWVLHDWSDSHCKVNLINKCYESLAKGKGIILIVESLIPVPE
		Qy	318 IDVIMLAHNPGKGERTEKEFALAKGAGFEGFRVASCANTWIEFLK

Qy 2 GSTSETKMSPSEAAMEEAAPVAMOLTSASVLPWVLSAELDVLIMAKAGPAHIST 61
 Db 16 GLTKESEOEIDEPKWMVSLQAESIV----NAVAPWVTKAALEGVIDTIAASNTWLSP 69
 Qy 62 SDIASLKLPTK--NPDAVMDRMKRLASVTCV---SLTLPDGKIERLYGLAVCK 115
 Db 70 SEIAVSLPKPTNPAPAVPULDRMURILVSHSILKCOMVERENGQTGKIRVYAEPICK 129
 Qy 116 FLTRNDGV-SIAALSLMNQDKVLMBSWHLTEAVLEGGLPPNKAQGMATFREYHTDPRF 174
 Db 130 YFLKQSDGSSLSLULLLSQVILKTWINKDQVILEGKQAFPSAAMDRLFEYISSDDQF 189
 Qy 175 NTVFENGMSHSTIMKKILETYKPGREGASWVYGGGTAHNMIAKPMKGINFDL 234
 Db 190 SKLFHRAMSESSSTMMKKVLUVEYRGDFDNTLVYGGGIGTILGLITSKYPHICGVNFDL 249
 Qy 235 PHVIEAPSPGVEMVGGDMVSVPKGDAFMKWCADMSDEHCKFLKCYEALPTNGK 294
 Db 250 AQLVLTQAPFVPGVKAVSGDMFVEPKGDAFMKWLHDWGEDCIIKILKNCWKS 309
 Qy 295 VILABGCILPVAP--DASLPPTKAVVHIDVIMLAHNPGKERTKEFEEALAKGAGPEFRV 351
 Db 310 VIVEMITPHEPKRNPSCNT--VLCMDLMLTQCSSGKERSLSQFENLAFAASPLCEI 367
 Qy 352 VASCAYNTWIEFLK 366
 Db 368 IC-LSVSYSVIEFHK 381

RESULT 15

F96044 hypothetical protein T5M16_11 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: F96044
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Hulka, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; Li, J.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani, C.A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Saizberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:1130712
 A;Accession: F96044
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-381 <STO>
 C;Genetics:
 A;Gene: T5M16_11
 C;Superfamily: O-methyltransferase
 C;Position: 1

Query Match 43.4%; Score 830.5; DB 2; Length 381;
 Best Local Similarity 45.5%; Pred. No. 2e-60; DB 16;
 Matches 168; Conservative 64; Mismatches 122; Inends 15; Gaps 6;
 Qy 9 MSPSEAAABEEAEEAVFVAMOLTSASVLPWVLSAELDVLIMAKAGPAHIST 61
 Db 17 LTKEESEOEIDEPKWMVSLQAESIV----NAVAPWVTKAALEGVIDTIAASNTWLSP 69
 Qy 69 PTK--NPDAVMDRMKRLASVTCV---SLTLPDGKIERLYGLAVCK 115
 Db 77 PTKPTNPEAVPULDRMURILVSHSILKCRMETGNGRT--GKTERVVAEPVCKYFLR 133
 Qy 120 NDDGV-SIAALSLMNQDKVLMBSWHLTEAVLEGGLPPNKAQGMATFREYHTDPRF 174
 Db 134 DSDGIGSLVLFMLHTQFVKTWNLKDVIEFDRDAFNSAHHMKIFETINSDDPFAELP 178
 134 DSDGIGSLVLFMLHTQFVKTWNLKDVIEFDRDAFNSAHHMKIFETINSDDPFAELP 173

Qy 179 NNGMSNHSTIMKKILETYKPGREGASWVYGGGTAHNMIAKPMK 179
 Db 194 NRAMSEBPTSTMKVKVLDVYGGDFEDNTLVYGGGNGTVLGIVLUTSKYPHK 194
 Qy 239 BEAPSYGVHGGGMFVSPKGDIAFMKWTCHMSDEHCKFLKFKKKYEA 239
 Db 254 TOAPFVPGVHGVSGDMFVEPKGDAFMKWTLDWGDDEDCKILKNCWKS 254
 Qy 299 ECILPVAP--DASLPPTKAVVHIDVIMLAHNPGKERTKEFEEALAKGAGPEFRV 299
 Db 314 EFVTPKPKGGDLSSNTVFMDDLMLTQCSSGKERSLSQFENLAFAASPLCEI 314
 Qy 358 NTWIEFLK 366
 Db 373 SSVIEFHK 381

Search completed: December 12, 2005, 08:38:10
 Job time : 42 secs

179 NNGMSNHSTIMKKILETYKPGREGASWVYGGGTAHNMIAKPMK
 194 NRAMSEBPTSTMKVKVLDVYGGDFEDNTLVYGGGNGTVLGIVLUTSKYPHK
 239 BEAPSYGVHGGGMFVSPKGDIAFMKWTCHMSDEHCKFLKFKKKYEA
 254 TOAPFVPGVHGVSGDMFVEPKGDAFMKWTLDWGDDEDCKILKNCWKS
 299 ECILPVAP--DASLPPTKAVVHIDVIMLAHNPGKERTKEFEEALAKGAGPEFRV
 314 EFVTPKPKGGDLSSNTVFMDDLMLTQCSSGKERSLSQFENLAFAASPLCEI
 358 NTWIEFLK 366
 373 SSVIEFHK 381

VI 238
 VI 253
 LA 298
 IV 313
 AY 357
 AY 372

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When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

If you have any questions regarding this information or your results, please contact any STIC searcher.

<http://www.dtr.uniproto.org/database/archive.shtml>

- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein archive database (UniPARC) at <http://www.dtr.uniproto.org/database/archive.shtml>
- Please note that the curators of the UniProt database purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- All of the sequence databases on ABS have recently been updated.

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RESULT 1

Q9SR00_LI-OST PRELIMINARY; PRT; 367 AA.

AC Q9SR00;

ID Q9SR00_LI-OST (Rel. 37, last sequence update)

AC Q9SR00;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-MAY-2004 (TREMBLrel. 26, last annotation update)

DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (COMT) (CADM)

DE methionine:caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-methionine:O-methyltransferase) (COMT) (CADM)

DE methionine:O-methyltransferase (EC 2.1.1.68) (S-adenosyl-methionine:O-methyltransferase) (COMT) (CADM)

GN Name=COMT;

OS Prunus dulcis (Almond) (Prunus amygdalus).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheobionta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus

OC Saxifragales; Hamamelidaceae; Liquidambar.

OC Speciayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC

OC Saxifragales; Hamamelidaceae; Liquidambar.

OX NCBI_TaxID:4400;

RN [1] _ TAXID:3755;

RN NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CV; TISSUE=Root;

RA Garcia-Mas J.; Messeguer R.; Arus P.; Puigdomenech P.;

RA Oakabe K.; Tsao C.C.; Li L.; Popko J.L.; Umezawa T.; Caraway D.T.,

RA Smeltzer R.H.; Joshi C.P.; Chiang V.L.;

RT "Coniferyl aldehyde 5-hydroxylation and methylation direct syringyl lignin biosynthesis in angiosperms";

RT Proc. Natl. Acad. Sci. U.S.A. 96:9545-9560 (1999).

DR EMBL; AFJ39533; ADA8913.1; -; mRNA.

DR HSSP; P28002; IYZ.

DR GO:0016206; P:catechol O-methyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR InterPro; IPR001601; Methytransferase.

DR InterPro; IPR00051; SAM bind.

DR InterPro; IPR011991; Wing_helix_DNA_bd.

DR Pfam; PF00891; Methyltransferase_2_1.

KW Methyltransferase; Transferase.

SEQ SEQUENCE 367 AA; 3F0SEB9BCB711779 CRC64;

Query Match 98.9%; Score 1894.5; DB 2; Length 367;

Best Local Similarity 99.5%; Pred. No. 1.9e-141; Mismatches 0; Indels 0; Gaps 0;

Matches 366; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

CC

QY 1 MGSTSETKMSSEAAAEEREEAFVAMQLTSSAVLPMVLUKSAIELDVLTEIMKAGRAHTS 60

1 MGSTSETKMSSEAAAEEREEAFVAMQLTSSAVLPMVLUKSAIELDVLTEIMKAGRAHTS 60

Db 61 TSDIASKLPTKPNPDAVMDLMLRLIASYSLTSURTLDGKTERLYGLAPVCKFLTRN 120

61 TSDIASKLPTKPNPDAVMDLMLRLIASYSLTSURTLDGKTERLYGLAPVCKFLTRN 120

Db 121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

Db 181 GMSNHSTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 240

181 GMSNHSTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 240

Db 241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

Db 241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

Db 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

Db 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFR-VALCAYNTW 359

Db 361 IIEFLKKI 368

361 IIEFLKKI 368

Db 360 IIEFLKKI 367

RESULT 2

COMT1_PRUDU STANDARD; PRT; 365 AA.

QY 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

QY 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

QY 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFR-VALCAYNTW 359

QY 179 GMADHISTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 238

179 GMADHISTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 238

QY 181 GMSNHSTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 240

181 GMSNHSTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 240

Db 121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

Db 119 BEGVSIAPLCLMLQNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 178

Db 59 PTDIASKLPTKPNPDAVMDLMLRLIASYSLTSURTLDGKTERLYGLAPVCKFLTRN 118

Db 61 TSDIASKLPTKPNPDAVMDLMLRLIASYSLTSURTLDGKTERLYGLAPVCKFLTRN 120

Db 61 TSDIASKLPTKPNPDAVMDLMLRLIASYSLTSURTLDGKTERLYGLAPVCKFLTRN 120

QY 121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

121 DDGVSTIAALSLMNQDKLMLMESWYHILTEAVLEGGLPPKNAVGMTAEYHGTDPRENTVNN 180

QY 179 GMADHISTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 238

179 GMADHISTITMKKILETYKGFFRGIGSYVWDVGGGTGAHNNMIAKYPWIKGINFDPHVIE 238

QY 241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

241 APSYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 300

QY 239 APQYGVVERHGGDMFVSPVKDAIFMKWICHWDSDPHCLKEPLKCYEALPQNGKYLAC 298

QY 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

QY 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

CC - TISSUE SPECIFICITY: Xylem.
 CC - PTM: The N-terminus is blocked.
 CC - SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
 CC - family. C01T subfamily.
 CC ---
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC ---
 CC EMBL; X62096; CAA44006.1; -; mRNA.
 DR EMBL; U3171; ARB61731.1; -; Genomic_DNA.
 DR PIR; S18568; S18568.
 DR HSSP; P28002; 1KYZ.
 DR SMR; Q0063; 5-364.
 DR InterPro; IPR012967; Dimerisation.
 DR InterPro; IPR008101; Methyltransfer.
 DR InterPro; IPR01077; O_Met_trans2.
 DR InterPro; IPR00051; SAM_bd.
 DR Pfam; PF0810; Dimerisation_1.
 DR Pfam; PF00891; Methyltransfer_2_1.
 DR Direct protein sequencing: lignin biosynthesis; Methyltransferase;
 KW Transf erase.
 SQ SEQUENCE 365 AA; 39805 MW; A6C8CDEA4E0007CD CRC64;

Query Match 83.3%; Score 1595.5; DB 1; Length 365;
 Best Local Similarity 80.9%; Pred. No. 8.9e-118; Indels 3; Gaps 2;
 Matches 297; Conservative 37; Mismatches 30; In dels 3; Gaps 2;

QY 1 MGSTSETKNSPSEAAAEEAFVAMQLTSAVLPVNLKSAIEDVLEMAKAGGAHIS 60
 Db 1 MGSTGTTQMTPTQ--VSDEEANHLFAMQLASVLPVNLKPAIEVDLEMAKAGGAPIS 58

QY 61 TSDIASKLPTKNPDAVMDRLMLRLASYSVTCSLRLTDGKIERLYGLAPVCKFLRN 120
 Db 59 TSEIASHLPLTPNPDARVMDLRILRLIASYSLTCSLKLDPGKVERLYGLAPVCKFLRN 118

QY 121 DDGVSTAALSLMNQDKVLMPSWYHTEAVLEGGIPFPNKAYGMATPRTYFVN 180
 Db 119 EDGVSTAALSLMNQDKVLMPSWYHTEAVLEGGIPFPNKAYGMATPRTYFVN 178

QY 181 GMSNHSITMKLILETYKFRGGLGSVWVGGTGAHNMIAKPMIKGINFDPHIVE 240
 Db 179 GMSNHSITMKLILETYKFRGGLGSVWVGGTGAHNMIAKPMIKGINFDPHIVE 238

QY 241 APSYGVHEVGGDMFVSPVKDAIFMKWICHWDSDHECLKFLKCYEALPTNGVTLAC 300
 Db 239 APSYGVHEVGGDMFVSPVKDAIFMKWICHWDSDHECLKFLKCYEALPTNGVTLAC 298

QY 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTERKEFEALAKGAGFEGFRWVACAYNTW 360
 Db 299 ILPVADASLPTKAVHIDVIMLAHNPGGKERTERKEFEALAKGAGFEGFRWVACAYNTW 357

QY 361 IIEFLKK 367
 Db 358 VIEFRKK 364

RESULT 5
 Q7X5J0 ROSCH
 ID Q7X5J0_ROSCH PRELIMINARY; PRT; 365 AA.
 AC 07X5J0;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DR Caffeic acid O-methyltransferase.
 GN Name=RCONM2;
 OS Rosa chinensis var. spontanea.
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Rosidae; Rosales; Rosaceae; Rosoideae; Fragaria.
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC Rosaceae; Rosoideae; Fragaria.
 QC ---

OX NCBITaxID=197613;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC TISSUE=Rose Flower petals;
 RA Wu S., Watanabe N., Mita S., Ueda Y., Shibuya M., Ebizuka Y
 RT "Two O-methyltransferases isolated from flower petals of Rose
 chinensis var. spontanea involved in scent biosynthesis.";
 RL J. Biosci. Bioeng. 0:0-0 (2003).
 RT EMBL; AB086104; BAC78827.1; -; mRNA.
 DR HSSP; P3524; 1FPI.
 SMR; P3524; 1FPI.
 DR InterPro; IPR01077; O_Met_trans2.
 DR InterPro; IPR00051; SAM_bd.
 DR Pfam; PF00891; Methyltransfer_2_1.
 DR Direct protein sequencing: lignin biosynthesis; Methyltransferase;
 KW Transf erase.
 SQ SEQUENCE 365 AA; 39669 MW; 2E46D4B039B65A70 CRC64;

Query Match 83.3%; Score 1595.5; DB 2; Length 365;
 Best Local Similarity 81.5%; Pred. No. 8.9e-118; Indels 300; Conservative 37; Mismatches 28; In dels 3; Gaps 2;

QY 1 MGSTSETKNSPSEAAAEEAFVAMQLTSAVLPVNLKSAIEDVLEMAKAGGAHIS 60
 Db 1 MGSTGTTQMTPTQ--VSDEEANHLFAMQLASVLPVNLKPAIEVDLEMAKAGGAPIS 58

QY 61 TSDIASKLPTKNPDAVMDRLMLRLASYSVTCSLRLTDGKIERLYGLAPVCKFLRN 120
 Db 59 PNDLQLSPLPTKNPAPVMDRLMLRLASYSVTCSLRLTDGKIERLYGLAPVCKFLRN 118

QY 121 DDGVSTAALSLMNQDKVLMPSWYHTEAVLEGGIPFPNKAYGMATPRTYFVN 180
 Db 119 EDGVSTAALSLMNQDKVLMPSWYHTEAVLEGGIPFPNKAYGMATPRTYFVN 178

QY 181 GMSNHSITMKLILETYKFRGGLGSVWVGGTGAHNMIAKPMIKGINFDPHIVE 240
 Db 179 GMSNHSITMKLILETYKFRGGLGSVWVGGTGAHNMIAKPMIKGINFDPHIVE 238

QY 241 APSYGVHEVGGDMFVSPVKDAIFMKWICHWDSDHECLKFLKCYEALPTNGVTLAC 300
 Db 239 APSYGVHEVGGDMFVSPVKDAIFMKWICHWDSDHECLKFLKCYEALPTNGVTLAC 298

QY 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTERKEFEALAKGAGFEGFRWVACAYNTW 360
 Db 299 ILPVADASLPTKAVHIDVIMLAHNPGGKERTERKEFEALAKGAGFEGFRWVACAYNTW 357

QY 361 IIEFLKK 367
 Db 358 VIEFRKK 365

RESULT 6
 Q9M602 FRAAN
 ID Q9M602_FRAAN PRELIMINARY; PRT; 365 AA.
 AC 09M602;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE O-methyltransferase.
 GN Name=omt1;
 OS Fragaria ananassa (Strawberry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Rosidae; Rosales; Rosaceae; Rosoideae; Fragaria.
 OC NCBI_TaxID=3747;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RA Kaldenhoff R., Wein M., Schwab W.;

RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR	AF220931; AF228333.1; -; mRN.
DR	EMBL; P28002; 1KYZ.
SNR;	0M602; 5-365.
GO;	GO:008171; P:S-adenosylmethionine-dependent methyltransf. . . ; IEA.
GO;	GO:0008171; P:S-adenosylmethionine-dependent methyltransf. . . ; IEA.
DR	InterPro; IPR016740; Methyltransf.
DR	InterPro; IPR010177; O-Met trans2.
DR	InterPro; IPR00051; SAM bFind.
DR	InterPro; IPR011991; Wing_hlx_DNA_bd.
DR	Pfam; PF00891; Methyltransf 2; 1.
KW	Methyltransferase; Transferase.
SEQUENCE	365 AA; 39817 MW; EF748P753B5550CB CRC64;
Query Match	83.0%; Score 1589.5; DB 2; Length 365;
Best Local Similarity	81.0%; Pred. No. 2.7e-117;
Matches	298; Conservative 39; Mismatches 28; Indels 3; Gaps 2;
QY	1 MGSTSETKSPSEAAEEAFVAMQTSASVLPVLUKSAILEDLEIMAKAGGAHTS 60
Db	1 MGSTGETQMTPTH -VSDEEANLFAFMQLASASVLPVLUKSAILEDLEIMAKAGFOSFLS 58
QY	61 TSDIASKUPLTPNPAVMDRMLLULASVSYLTSCLSLRTLDGKIRLYGLAPVCPFLRN 120
Db	59 PSDLASQPLTPNPERPVLMLDRMLLULASVILTSCLSLRTLDGKIRLYGLAPVCPFLRN 118
QY	121 DGSVSIALLSLMNQDKVLMESWYHTEAVLEGPIPNKAYGMATFEGHDPRFTVFN 180
Db	119 EGDVSIALLCLMNQDKVLMESWYHTEAVLEGPIPNKAYGMATFEGHDPRFTVFN 178
QY	181 GMSNHSTIMKKILETYKGFEGLGSWVGGTGAAHNNIIAKUPMIKGNFDLPHVIE 240
Db	179 GMDHSTITMKKILETYKGFEGLGSWVGGTGAAHNNIIAKUPMIKGNFDLPHVIE 238
QY	241 APSYYPGVHVGGMFVSVVKGDARFMWKWCHDWSDEHCLFLKCKYEAALPINKTIAEC 300
Db	239 APQYGPGVHVGGMFVSVVKGDARFMWKWCHDWSDEHCLFLKCKYEAALPINKTIAEC 298
QY	301 ILVPVADSLPLTPKAVWHIDVIMLAHNPGKERTKEFEALAKGAGPGEGRVVASCAINTW 360
Db	299 ILVPVADSLPLATKGVWHIDVIMLAHNPGKERTKEFEALAKGSGFOQIRVCCD-AFNTY 357
QY	361 IIEFLKK 368
Db	358 VIEFLKK 365
RESULT 7	
COMT1_POKI	
ID	COMT1_POKI STANDARD; PRT; 365 AA.
AC	Q43046;
DT	10-OCT-2003 (rel. 42, Created)
DT	10-OCT-2003 (rel. 42, Last sequence update)
DT	10-MAY-2005 (rel. 47, Last annotation update)
DE	Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (CAOMT-1). Name=COMT1; Name=CAOMT1;
OS	Populus kitakamensis (Aspen).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; NCBI_TaxID=368;
RN	[1] NUCLEOTIDE SEQUENCE.
RA	Hayakawa T., Nanto K., Kawai S., Katayama Y., Morohoshi N.; "Molecular cloning and tissue-specific expression of two genes that encode caffeic acid O-methyltransferases from <i>Populus kitakamensis</i> ."; <i>Plant Sci.</i> 113:157-165(1996).
RT	-I- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.
RESULT 8	
ID	Q9M569_9ROSTI
AC	Q9M569_9ROSTI PRELIMINARY;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Caffeic acid 3-O-methyltransferase (Fragment).
GN	Name=COMT;
OS	<i>Populus tomentosa</i> .
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; NCBI_TaxID=18781;

CC	- I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone = S-adenosyl-methionine + 3-methoxy-4-hydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone.
CC	cinnamate. cinnamate = S-adenosyl-methionine + 3-methoxy-4-hydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone.
CC	- I- PATHWAY: Lignin biosynthesis.
CC	EMBL: M73431; ARB60951.1; -; mRNA.
DR	HSSP: P28002; IKY2.
DR	DR GO: GO:0008171; F:O-methyltransferase activity; IEA.
DR	GO: GO:000857; F:S-adenosylmethionine-dependent methyltransf. . . ; IEA.
DR	DR GO: GO:0016740; F:transferase activity; IEA.
DR	DR InterPro: IPR01601; Methyltransf.
DR	DR InterPro: IPR01077; O Met transf.
DR	DR InterPro: IPR00051; SAM-bind.
DR	DR InterPro: IPR01991; Wing-helix DNA bd.
KW	Methyltransferase; Transferase.
FT	FT Pfam: PF00891; Methyltransferase; 2.
FT	Methyltransferase; Transferase.
NON_TER	NON_TER 360
SEQUENCE	SEQUENCE 360 AA: 39174 MW: 40AC6D8EF1C1243D CRC64;
Query	Query Match 82.5%; Score 1579.5; DB 2; Length 360;
Matches	Best Local Similarity 81.0%; Pred. No. 1.6e-116; Mismatches 294; Conservative 36; Indels 3; Gaps 2;
Qy	Qy 1 MGSTSETKMSPEAAAEAEAVFAMQLTSASVLPVNLQSALETDVLEIMAKAGPRAHTS 60
Db	Db 1 MGSTGETQMTPTQ- VSDEERHLFAMQASVLPMLKTAIELDIEMAKAGPRAHTS 58
Qy	Qy 61 TSDIASKLPTKNDPDAVMDRMLRLLASVLTCSRTLPKGKIEBLGLAPVCKLTRN 120
Db	Db 59 TSEFASHLPTKNDPDAVMDRDLRLLASVLTCSRLPDKGKIEBLGLAPVCKLTRN 118
Qy	Qy 121 DDGVSIAALSLMNQDQVLMESWYHTEAVLGGIPNKAGMTAFYHGTBRENTYFN 180
Db	Db 119 EDGVSVSPCLMNQDQVLMESWYHTEAVLGGIPNKAGMTAFYHGTBRENTYFN 178
Qy	Qy 181 GMSNHTTITMKKILETYKGPEGIGSVWVGGTGAVENTVSKYPSIGI 240
Db	Db 179 GMSDHSITTIMKKILETYKGPEGIGSVWVGGTGAVENTVSKYPSIGI 238
Qy	Qy 241 APSYCPGVHVGDMFVSPVKDAIFMKWICHDSBDEHCKLKEKKCTEAALPTNGKVIAEC 300
Db	Db 239 APSYCPGVHVGDMFVSPVKDAFVKWICHDSDAHCKLKEKKCTDALPENGKVILVE 298
Qy	Qy 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALKGAGFEGFRVAVASCNTW 360
Db	Db 299 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALKGAGFEGFRVAVASCNTW 357
Qy	Qy 361 IIE 363
Db	Db 358 VIE 360
RESULT 9	RESULT 9
Q9LWB8_9ROSI	Q9LWB8_9ROSI PRELIMINARY; PRT; 364 AA.
ID	ID Q9LWB8_9ROSI
AC	AC Q9LWB8_9ROSI
DT	DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT	DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT	DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE	DE O-methyltransferase.
OS	OS Populus deltoides.
OC	OC Populus trichocarpa x Populus deltoides.
OC	OC Bokarvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
OC	OC OCBT - TaxID:3695;
RN	RN [1]
NC	NC NUCLEOTIDE SEQUENCE.
RC	RC Dumas B., Van Doorslaere J., Legrand M., Van Montagu M.M., Inze D.; Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RC	RC -I- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding
RA	RA [1]
RA	RA NUCLEOTIDE SEQUENCE.
RC	RC STRAIN=cv. Apollo;
RC	RC Gori G., Bugos R.C., Campbell W.H., Maxwell C.A., Dixon R.J.
RA	RA Medicago sativa (Alfalfa).
RC	RC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Fabales; Papilionoideae; Trifolaceae; Fabaceae.
RC	RC NUBI_TaxID:3879;
RN	RN [1]
NC	NC NUCLEOTIDE SEQUENCE.
CC	CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone = S-adenosyl-methionine + 3-methoxy-4-hydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone.
CC	CC cinnamate. cinnamate = S-adenosyl-methionine + 3-methoxy-4-hydroxy-5-hydroxy-6-methyl-2H,4H-1,2-dihydro-3,4-dihydro-5H-furanone.
CC	CC - I- PATHWAY: Lignin biosynthesis.
CC	CC EMBL: M73431; ARB60951.1; -; mRNA.
DR	DR HSSP: P28002; IKY2.
DR	DR GO: GO:0008171; F:O-methyltransferase activity; IEA.
DR	DR GO: GO:000857; F:S-adenosylmethionine-dependent methyltransf. . . ; IEA.
DR	DR GO: GO:0016740; F:transferase activity; IEA.
DR	DR InterPro: IPR01601; Methyltransf.
DR	DR InterPro: IPR01077; O Met transf.
DR	DR InterPro: IPR00051; SAM-bind.
DR	DR InterPro: IPR01991; Wing-helix DNA bd.
KW	KW Methyltransferase; Transferase.
FT	FT Pfam: PF00891; Methyltransferase; 2.
FT	Methyltransferase; Transferase.
NON_TER	NON_TER 360
SEQUENCE	SEQUENCE 364 AA: 39724 MW: 033287806443CD9 CRC64;
SQ	SQ SEQUENCE 364 AA: 39724 MW: 033287806443CD9 CRC64;
Query	Query Match 82.4%; Score 1578.5; DB 2; Length 3;
Matches	Best Local Similarity 80.6%; Pred. No. 2.6e-116; Mismatches 295; Conservative 36; Indels 32; Gaps 2;
Qy	Qy 1 MGSTSETKMSPEAAAEAEAVFAMQLTSASVLPVNLQSALETDVLEIMAKAGPRAHTS 60
Db	Db 1 MGSTGETQMTPTQ- VSDEERHLFAMQASVLPMLKTAIELDIEMAKAGPRAHTS 58
Qy	Qy 61 TSDIASKLPTKNDPDAVMDRMLRLLASVLTCSRTLPKGKIEBLGLAPVCKLTRN 120
Db	Db 59 TSEFASHLPTKNDPDAVMDRDLRLLASVLTCSRLPDKGKIEBLGLAPVCKLTRN 118
Qy	Qy 121 DDGVSIAALSLMNQDQVLMESWYHTEAVLGGIPNKAGMTAFYHGTBRENTYFN 180
Db	Db 119 EDGVSVSPCLMNQDQVLMESWYHTEAVLGGIPNKAGMTAFYHGTBRENTYFN 178
Qy	Qy 181 GMSNHTTITMKKILETYKGPEGIGSVWVGGTGAVENTVSKYPSIGI 240
Db	Db 179 GMSDHSITTIMKKILETYKGPEGIGSVWVGGTGAVENTVSKYPSIGI 238
Qy	Qy 241 APSYCPGVHVGDMFVSPVKDAIFMKWICHDSBDEHCKLKEKKCTEAALPTNGKVIAEC 300
Db	Db 239 APSYCPGVHVGDMFVSPVKDAFVKWICHDSDAHCKLKEKKCTDALPENGKVILVE 298
Qy	Qy 301 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALKGAGFEGFRVAVASCNTW 360
Db	Db 299 ILPVADASLPTKAVVHIDVIMLAHNPGGKERTKEFEALKGAGFEGFRVAVASCNTW 357
Qy	Qy 361 IIE 363
Db	Db 358 VIE 363
RESULT 10	RESULT 10
CONT1	CONT1 MEDSA
CONT1	CONT1 MEDSA STANDARD; PRT; 365 AA.
ID	ID P28002;
AC	AC P28002;
DT	DT 01-AUG-1992 (Rel. 23, Created)
DT	DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT	DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE	DE Coffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM:Medicago sativa (Alfalfa))
OS	OS Bokarvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Fabales; Papilionoideae; Trifolaceae; Fabaceae.
OC	OC Medicago sativa (Alfalfa).
OC	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Malpighiales; Salicaceae; Populus.
OC	OC OCBT - TaxID:3879;
RN	RN [1]
NC	NC NUCLEOTIDE SEQUENCE.
RC	RC STRAIN=cv. Apollo;
RC	RC Gori G., Bugos R.C., Campbell W.H., Maxwell C.A., Dixon R.J.

RT	"Stress responses in alfalfa (<i>Medicago sativa</i> L.). X. Molecular cloning and expression of S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase, a key enzyme of lignin biosynthesis.";
RL	Plant Physiol. 97:7-14 (1991).
CC	-i- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.
CC	-i- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-cinnamate.
CC	-i- TISSUE SPECIFICITY: More abundant in roots and stems.
CC	-i- INDUCTION: By infection, plant wounding, or elicitor treatment of cell cultures.
CC	-i- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2 family. COMT subfamily.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	EMBL: M63853; AAB46623; 1; -; mRNA.
DR	PIR: T09673; T09573.
DR	PDB: 1KWM; X-ray; A/C/F=1-365.
DR	PDB: 1KYZ; X-ray; A/C/F=1-365.
DR	InterPro: IPR012867; Dimerisation.
DR	InterPro: IPR01601; Methyltransfer.
DR	InterPro: IPR01077; O Met trans2.
DR	InterPro: IPR00051; SAM bd.
DR	InterPro: IPR01991; Wing_helix_DNA_bd.
DR	Pfam: PF08100; Dimerisation; I.
KW	3D-structure; Lignin biosynthesis; Methyltransferase; Transferase.
FT	HELIX 16 27
FT	TURN 28 30
FT	HELIX 31 41
FT	TURN 42 43
FT	HELIX 44 49
FT	TURN 50 51
FT	TURN 53 54
FT	STRAND 57 59
FT	HELIX 65 66
FT	TURN 71 72
FT	HELIX 73 86
FT	TURN 87 88
FT	STRAND 90 96
FT	TURN 98 99
FT	STRAND 102 108
FT	HELIX 110 115
FT	TURN 119 120
FT	TURN 124 125
FT	HELIX 125 131
FT	TURN 132 137
FT	HELIX 134 137
FT	HELIX 138 142
FT	HELIX 143 149
FT	HELIX 153 158
FT	HELIX 162 165
FT	HELIX 166 168
FT	HELIX 170 194
FT	TURN 197 198
FT	STRAND 203 207
FT	TURN 208 209
FT	TURN 210 211
FT	HELIX 213 221
FT	TURN 223 224
FT	STRAND 226 231
FT	TURN 233 238
FT	TURN 243 244
RESULT 11	
COMT1_BUCCU	
ID	COMT1_BUCCU
AC	P46434;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM)
DB	Name=COMT;
OS	Eucalyptus gunnii (Cider tree).
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; Magnoliopsida; eudicots; core eudicots
OC	Spermatophyta; Magnoliopsida; eudicots; eudicots; core eudicots
OC	rosids; Myrtales; Myrtaceae; Eucalyptus.
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Xylem;
RC	MEDLINE=93345011; PubMed=8066135; DOI=10.1104/PP.1.05.2.749;
RA	Poeymbre O.; Bouet A.M.; Grima-Pettinatti J.;
RT	"A cDNA encoding S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase from Eucalyptus."
RL	Plant Physiol. 105:749-750 (1994).
CC	-i- FUNCTION: Catalyzes the conversion of caffeic acid to sinapic acid and of 5-hydroxyferulic acid to sinapic acid. The result

cid	3	2;
	IS	60
	IS	58
	RN	120
	:	
	KN	118
	NN	180
	NK	178
	EE	240
	ED	238
	EC	300
	EC	298
	TW	360
	TY	357

use as long as its content is in no way modified and this is not removed.

CC 1 MGSTGNAETQLTPTH--VSDEEANLFAMQLASASVLPVMVKAATBLDVBLIMAKSIPHGS 58

CC 56 GAHHTSDTAKSLPKTPKNPDAVMRMLRLASASVLTCSLRTIPDGKBERLIGLAPVCK 115

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 59 GAYTSPAEITAAQOLPTNPAPVMDRVRLLASSTSVTWSLREPDGKVERLIGLAPVCK 118

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 116 PLTNRNDGGSIAAALSLMNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 175

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 119 PLTNQEDGVSLSLAPCLMLNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 178

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 176 TVEFNGMSNHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 235

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 179 KVFRGMSDHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 238

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 296 ILAECLIPVAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVVASC 355

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 299 IVACELPLSPDPLATKGVHIDAIMLAHNPGGKERTKEFEALAIAGAGFTGK-VACC 357

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 356 AYNTWIEFIK 366

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 358 AFNTVMEFLK 368

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

RESULT 13

COMT1_CBARAN STANDARD; PRT; 359 AA.

ID COMT1_CBARAN STANDARD; PRT; 359 AA.

AC Q9PQY8; P93098; 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).

DE Name=COMT;

GN Capsicum annuum (Bell pepper);

OS Capsicaceae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; Asterids; Lamiales; Solanales; Solanaceae; Capsicum.

NCBI_TaxID=4072;

[1]

RN 301 ILPVAAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFR

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=pericarp;

RA Lee B.-H., Choi D., Lee K.-W.:

RT "Isolation and characterization of o-diphenol-O-methyltransferase cDNA from hot pepper (Capsicum annuum L.)", J. Plant Biol. 41:9-14(1998).

RL [2]

RN 302 ILPVAAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFR

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CV; Chungyang; TISSUE=Root;

RA Kim K.-W., Lee S.-W.:

RT "Isolation and characterization of caffeic acid O-methyltransferase cDNA from Capsicum annuum.", Submitted (DDBJ-1999) to the EMBL/GenBank/DBJ databases.

-I- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-cinnamate.

-I- PATHWAY: Lignin biosynthesis.

-I- TISSUE SPECIFICITY: Fruit. Not expressed in leaf, but decreases during ripening.

-I- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2 family. COMT subfamily.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this is not removed.

CC 1 MGSTGNAETQLTPTH--VSDEEANLFAMQLASASVLPVMVKAATBLDVBLIMAKSIPHGS 58

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 56 GAHHTSDTAKSLPKTPKNPDAVMRMLRLASASVLTCSLRTIPDGKBERLIGLAPVCK 115

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 59 GAYTSPAEITAAQOLPTNPAPVMDRVRLLASSTSVTWSLREPDGKVERLIGLAPVCK 118

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 116 PLTNRNDGGSIAAALSLMNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 175

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 119 PLTNQEDGVSLSLAPCLMLNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 178

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 176 TVEFNGMSNHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 235

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 179 KVFRGMSDHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 238

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 296 ILAECLIPVAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVVASC 355

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 299 IVACELPLSPDPLATKGVHIDAIMLAHNPGGKERTKEFEALAIAGAGFTGK-VACC 357

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 356 AYNTWIEFIK 366

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 358 AFNTVMEFLK 368

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

RESULT 13

COMT1_CBARAN STANDARD; PRT; 359 AA.

ID COMT1_CBARAN STANDARD; PRT; 359 AA.

AC Q9PQY8; P93098; 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).

DE Name=COMT;

GN Capsicum annuum (Bell pepper);

OS Capsicaceae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; Asterids; Lamiales; Solanales; Solanaceae; Capsicum.

NCBI_TaxID=4072;

[1]

RN 301 ILPVAAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFR

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=pericarp;

RA Lee B.-H., Choi D., Lee K.-W.:

RT "Isolation and characterization of o-diphenol-O-methyltransferase cDNA from hot pepper (Capsicum annuum L.)", J. Plant Biol. 41:9-14(1998).

RL [2]

RN 302 ILPVAAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFR

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CV; Chungyang; TISSUE=Root;

RA Kim K.-W., Lee S.-W.:

RT "Isolation and characterization of caffeic acid O-methyltransferase cDNA from Capsicum annuum.", Submitted (DDBJ-1999) to the EMBL/GenBank/DBJ databases.

-I- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-cinnamate.

-I- PATHWAY: Lignin biosynthesis.

-I- TISSUE SPECIFICITY: Fruit. Not expressed in leaf, but decreases during ripening.

-I- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2 family. COMT subfamily.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this is not removed.

CC 1 MGSTGNAETQLTPTH--VSDEEANLFAMQLASASVLPVMVKAATBLDVBLIMAKSIPHGS 58

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 56 GAHHTSDTAKSLPKTPKNPDAVMRMLRLASASVLTCSLRTIPDGKBERLIGLAPVCK 115

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 59 GAYTSPAEITAAQOLPTNPAPVMDRVRLLASSTSVTWSLREPDGKVERLIGLAPVCK 118

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 116 PLTNRNDGGSIAAALSLMNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 175

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 119 PLTNQEDGVSLSLAPCLMLNQDKVLMSWYHTEAVLEGGLPPFKAYGMATPEYHGTDPREN 178

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 176 TVEFNGMSNHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 235

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

CC 179 KVFRGMSDHTIMKILKLYTKEFEGLGSWSVWYQGGTGAHLLNMIAKYPMIKINFDP 238

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 296 ILAECLIPVAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVVASC 355

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 299 IVACELPLSPDPLATKGVHIDAIMLAHNPGGKERTKEFEALAIAGAGFTGK-VACC 357

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

QY 356 AYNTWIEFIK 366

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

Db 358 AFNTVMEFLK 368

CC ||::|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:|| :||:||

RESULT 14

COMT1_OCTBA STANDARD; PRT; 361 AA.

ID COMT1_OCTBA STANDARD; PRT; 361 AA.

AC Q9XK00; P93098; 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1)

DE Name=COMT1;

GN Ocimum basilicum (Sweet basil).

OS Ocimum basilicum (Sweet basil);

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamids; Lamiales; Solanales; Solanaceae; Nepetoideae; Ocineae

NCBI_TaxID=39350;

[1]

RN 301 ILPVAAPDASILPTKAVHVDVIMLAHNPGGKERTKEFEALAKGAGFEGFR

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CV; EMK-1;

RA Wang J., Dudareva N., Kish C.M., Simon J.E., Lewinsohn E., Pichersky E.;

RT "Nucleotide sequences of two cDNAs encoding caffeic acid O-

^ Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rup

ge 11

Db 357 VIEFRHQ 363

Search completed: December 12, 2005, 08:37:26
Job time : 234 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.		29	500.5	26.1	174	2	US-09-971-823B-27	Seq	Appl
Run on: December 12, 2005, 08:30:15 ; Search time 46 Seconds		30	47.9	25.0	198	2	US-09-615-192A-271	Seq	Appl
Scoring table: BLOSUM62		31	413.5	21.6	156	2	US-09-615-192A-272	Seq	Appl
Scored: Gapop 10.0 , Gapext 0.5		32	376.5	19.7	160	2	US-09-615-192A-275	Seq	Appl
Searched: 572060 seqs, 82675679 residues		33	372	19.4	188	2	US-09-500-569-8	Seq	Appl
Total number of hits satisfying chosen parameters: 572060		34	372	19.4	145	2	US-09-615-192A-270	Seq	Appl
Minimum DB seq length: 0		35	365	19.1	94	1	US-08-266-451B-20	Seq	Appl
Maximum DB seq length: 200000000		36	356.5	18.6	1	US-08-748-725-20	Seq	Appl	
Post-processing: Minimum Match 0% Listing first 100 summaries		37	356	18.6	43	2	US-09-971-823B-24	Seq	Appl
Database : Issued Patents AA,*		38	291.5	15.2	313	2	US-09-903-540-9934	Seq	Appl
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3: /cgn2_6/pctdata/1/iaa/H_COMBO_PEP:*		41	254.5	13.3	332	2	US-09-721-797-18	Seq	Appl
4: /cgn2_6/pctdata/1/iaa/PCTUS_COMBO_PEP:*		42	249.5	13.0	351	2	US-09-266-965-133	Seq	Appl
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6: /cgn2_6/pctdata/1/iaa/backfile1.pep:*		44	226	11.8	49	4	US-09-509-522-3	Seq	Appl
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		47	212.5	11.1	621	2	US-09-265-965-4	Seq	Appl
		48	212.5	11.1	621	2	US-09-382-522-1	Seq	Appl
		49	211.5	11.0	452	2	US-09-509-522-3	Seq	Appl
		50	211.5	11.0	452	2	US-09-389-527-3	Seq	Appl
		51	186.5	9.7	356	1	US-08-959-941-2	Seq	Appl
		52	186.5	9.7	109	2	US-09-501-569-22	Seq	Appl
		53	173	9.0	115	2	US-09-259-924-2	Seq	Appl
		54	171.5	9.0	123	2	US-09-500-569-28	Seq	Appl
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		56	166.5	8.7	109	2	US-09-501-569-22	Seq	Appl
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		58	147.5	7.7	117	2	US-09-266-965-5	Seq	Appl
		59	146	7.6	125	2	US-09-265-965-3	Seq	Appl
		60	141	7.4	125	2	US-09-902-500-10705	Seq	Appl
		61	112.5	5.9	368	2	US-09-252-991A-20452	Seq	Appl
		62	107	5.6	139	2	US-09-252-991A-17621	Seq	Appl
		63	100.5	5.2	308	1	US-08-457-245-8	Seq	Appl
		64	91.5	4.8	237	1	US-08-576-626A-58	Seq	Appl
		65	91	4.8	379	2	US-09-489-039A-12857	Seq	Appl
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		67	89.5	4.7	482	2	US-09-252-991A-17621	Seq	Appl
		68	89	4.6	578	2	US-09-489-039A-14097	Seq	Appl
		69	89	4.6	902	2	US-09-949-016-961	Seq	Appl
		70	88.5	4.6	522	2	US-09-902-540-12872	Seq	Appl
		71	86.5	4.5	437	2	US-09-603-777A-84	Seq	Appl
		72	86	4.5	439	2	US-09-134-00C-6557	Seq	Appl
		73	86	4.5	483	2	US-09-378-3-131	Seq	Appl
		74	85.5	4.5	603	1	US-09-681-865A-2	Seq	Appl
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		82	84	4.4	897	2	US-09-543-681A-4249	Seq	Appl
		83	83	4.3	510	2	US-09-801-344-8	Seq	Appl
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		88	82	4.3	803	1	US-09-362-368-4	Seq	Appl
		89	81.5	4.3	609	2	US-09-115-475-19	Seq	Appl
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		93	81.5	4.3	3144	1	US-09-246-982-6	Seq	Appl
		94	81.5	4.3	3144	1	US-09-453-265-6	Seq	Appl
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		96	81.5	4.3	3144	2	US-09-556-419-21	Seq	Appl
		97	81.5	4.3	3144	2	US-09-041-886-15	Seq	Appl
		98	81.5	4.3	3144	2	US-09-538-092-1118	Seq	Appl
		99	4.2	3144	2	US-09-724-797-14	Seq	Appl	
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		2	328	2	US-09-615-192A-274	Seq	Appl		
		27	667	2	US-09-134-001C-3624	Seq	Appl		

ALIGNMENTS

RESULT 1
 US-08-91-677-6
 ; Sequence 6, Application US/08991677A
 ; Patent No. 6252135
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiang, Vincent L
 ; APPLICANT: Carraway, Daniel T
 ; APPLICANT: Smelzler, Richard H
 ; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
 ; CURRENT APPLICATION NUMBER: US/08/991,677A
 ; CURRENT FILING DATE: 1997-12-16
 ; EARLIER APPLICATION NUMBER: US 60/033,381
 ; EARLIER FILING DATE: 1996-12-16
 ; SOFTWARE: patentin ver. 2.0
 ; SEQ ID NO: 6
 ; LENGTH: 368
 ; TYPE: PRT
 ; ORGANISM: Liquidambar styraciflua
 ; US-08-91-677-6

Query Match 100.0%; Score 1915; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1.9e-204; Mismatches 0; Indels 0; Gaps 0;
 Matches 368; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTSETKMPSEAAAEAEAAVFAVAMOLTSASVLPNVKSAEIDVLEIMAKAGPGAHIS 60
 Db 1 MGSTSETKMPSEAAAEAEAAVFAVAMOLTSASVLPNVKSAEIDVLEIMAKAGPGAHIS 60

QY 61 TSDIASKLPTKNPDAVMDMLRLASVLTCSLRTPDGKLERLYGLAPVCKFLTRN 120
 Db 61 TSDIASKLPTKNPDAVMDMLRLASVLTCSLRTPDGKLERLYGLAPVCKFLTRN 120

QY 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPPNKAYGTMATEYHGDPRYTFNN 180
 Db 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPPNKAYGTMATEYHGDPRYTFNN 180

QY 181 GMSNHSTITMKKILETYKGFFGLGSVWVGGGTGAHLNMTIAYKPMIGNFDLPHVIE 240
 Db 181 GMSNHSTITMKKILETYKGFFGLGSVWVGGGTGAHLNMTIAYKPMIGNFDLPHVIE 240

QY 241 APSYRGVERVGGDMFVSPVKDAIFMKWICHDDSDHECLPKYCBEALTTNGKYLABC 300
 Db 241 APSYRGVERVGGDMFVSPVKDAIFMKWICHDDSDHECLPKYCBEALTTNGKYLABC 300

QY 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360
 Db 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

QY 361 IIEFLKKI 368
 Db 361 IIEFLKKI 368

RESULT 2
 US-08-715-325-2
 ; Sequence 2, Application US/08715325
 ; Patent No. 5886243
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiang, Vincent L
 ; APPLICANT: Tsai, Chung-Jui
 ; APPLICANT: Podia, Gopi
 ; TITLE OF INVENTION: Genetic Engineering of Wood Color
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Michael, Best & Friedrich

STREET: 100 E. Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: United States of America
 ZIP: 53202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS 6.22
 SOFTWARE: WordPerfect for Windows 5.2

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/715,325
 FILING DATE: 30 NOV 1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US60/007727
 FILING DATE: 30 NOV 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Gemignani, Joseph A
 REGISTRATION NUMBER: 19,482
 NUMBER OF SEQ ID NOS: 11
 REFERENCE/DOCKET NUMBER: 66040/9627

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 271-6560
 TELEFAX: (414) 277-0656

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 HYPOTHETICAL: no

QY 1 MGSTSETKMPSEAAAEAEAAVFAVAMOLTSASVLPNVKSAEIDVLEIMAKAGPGAHIS 60
 Db 1 MGSTSETKMPSEAAAEAEAAVFAVAMOLTSASVLPNVKSAEIDVLEIMAKAGPGAHIS 60

QY 61 TSDIASKLPTKNPDAVMDMLRLASVLTCSLRTPDGKLERLYGLAPVCKFLTRN 120
 Db 61 TSDIASKLPTKNPDAVMDMLRLASVLTCSLRTPDGKLERLYGLAPVCKFLTRN 120

QY 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPPNKAYGTMATEYHGDPRYTFNN 180
 Db 121 DDGVSTAALSLMNQDKVLMESWYHTEAVLEGGLIPPNKAYGTMATEYHGDPRYTFNN 180

QY 181 GMSNHSTITMKKILETYKGFFGLGSVWVGGGTGAHLNMTIAYKPMIGNFDLPHVIE 240
 Db 181 GMSNHSTITMKKILETYKGFFGLGSVWVGGGTGAHLNMTIAYKPMIGNFDLPHVIE 240

QY 241 APSYRGVERVGGDMFVSPVKDAIFMKWICHDDSDHECLPKYCBEALTTNGKYLABC 300
 Db 241 APSYRGVERVGGDMFVSPVKDAIFMKWICHDDSDHECLPKYCBEALTTNGKYLABC 300

QY 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360
 Db 301 ILPVADASLPTKAVHIDVIMLAHNPGGKERTKEFEALAKGAGFEGFRVASCAYNTW 360

QY 361 IIEFLKKI 368
 Db 361 IIEFLKKI 368

RESULT 3
 US-09-947-027-6
 ; Sequence 6, Application US/09947027
 ; Patent No. 6855864
 ; GENERAL INFORMATION:

APPLICANT: Chiang, Vincent Lee C.
 TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
 FILE REFERENCE: 060-0-9718
 CURRENT APPLICATION NUMBER: US/09/947, 027
 FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: 60/230, 086
 PRIORITY DATE: 2000-09-05
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 6
 LENGTH: 365
 TYPE: PRT
 ORGANISM: abpen populus tremuloides
 US-09-947-6

Query Match 83.3%; Score 1595.5; DB 2; Length 365;
 Best Local Similarity 80.9%; Pred. No. 7.8e-169; Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSTSETKNSPSEAAAEERAFVAMOLTSASVLPMLVKAIELVLEWAKAGPAGHS 60
 Db 1 MGSTGETQMPHQ--VSDEBAHLFAMQLASVLPMLVKAIELVLEWAKAGPAGHS 58

Qy 61 TSDIAKLPPTKNPDAVMFLRMLRLLASYSVTCSLRTLPDKGIERLYGLAPVCKFLTRN 120
 Db 59 TSEASHLHPTKNPDAVFLDRILRLLASYSVTCSLKDLPDGKVERLYGLAPVCKFLTKN 118

Qy 121 DDGVSTAALSLMNQKVLMSWYHLTEAVLLEGGLPFPKAGMTAFEYKGDPRFTVNN 180
 Db 119 EDGVVSPLCIMNQDKVLMESWYHLTEAVLLEGGLPFPKAGMTAFEYKGDPRFTVNN 178

Qy 181 GMSNSTITMKKILETYKGREGGLSVDVGGTGAHLNMTAKYMIKGINFDPHIVE 240
 Db 179 GMSNSTITMKKILETYKGREGGLSVDVGGTGAHLNMTAKYMIKGINFDPHIVE 238

Qy 241 APSYGVVERVGGDMFVSPKGDATFMKWTCHDMSDBECHLKLKCYEALP 300
 Db 239 APSYGVVERVGGDMFVSPKGDATFMKWTCHDMSDBECHLKLKCYDLP 298

Qy 301 ILPVARDASILPTKAVHIDIMLAINPGGKERTERKEFALKAGAFREGFGRVVAQNTW 360
 Db 299 ILPVARDASILPTKAVHIDIMLAINPGGKERTERKEFALKAGAFQGEVNC-CAENTH 357

Qy 361 IIEFLKK 367
 Db 358 VIEFRKK 364

RESULT 4
 US-08-204-288-2

; Sequence 2, Application US/08204288
 ; GENERAL INFORMATION:
 ; Patent No. 5959178
 ; APPLICANT: VAN DOORSELARE, Jan
 ; APPLICANT: FOTIG, Bernard J.M.
 ; APPLICANT: INZE, Dirk G.
 ; APPLICANT: JOURNIN, Lise
 ; APPLICANT: KNIGHT, Mary E.
 ; APPLICANT: VAN MONTAGU, Marc
 ; APPLICANT: LAGRAND, Michel
 ; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
 ; TITLE OF INVENTION: PLANTS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3518
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/204, 288
 FILING DATE: 10-MAR-1994
 CLASIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9119279.9
 FILING DATE: 10-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/01460
 FILING DATE: 09-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, Paul N.
 REGISTRATION NUMBER: 16, 773
 REFERENCE/DOCKET NUMBER: 206860/SEB36543/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-204-288-2

Query Match 82.1%; Score 1572.5; DB 1; Length 3;
 Best Local Similarity 80.3%; Pred. No. 2.8e-166; Matches 294; Conservative 36; Mismatches 33; Indels 2;

Qy 1 MGSTSETKNSPSEAAAEERAFVAMOLTSASVLPMLVKAIELVLEWAKAGPAGHS 60
 Db 1 MGSTGETQMPHQ--VSDEBAHLFAMQLASVLPMLVKAIELVLEWAKAGPAGHS 58

Qy 61 TSDIAKLPPTKNPDAVMFLRMLRLLASYSVTCSLRTLPDKGIERLYGL 120
 Db 59 TSEASHLHPTKNPDAVFLDRILRLLASYSVTCSLKDLPDGKVERLYGL 118

Qy 121 DDGVSTAALSLMNQKVLMSWYHLTEAVLLEGGLPFPKAGMTAFEYKGDPRFTVNN 180
 Db 119 EDGVVSPLCIMNQDKVLMESWYHLTEAVLLEGGLPFPKAGMTAFEYKGDPRFTVNN 178

Qy 181 GMSNSTITMKKILETYKGREGGLSVDVGGTGAHLNMTAKYMIKGINFDPHIVE 240
 Db 179 GMSNSTITMKKILETYKGREGGLSVDVGGTGAHLNMTAKYMIKGINFDPHIVE 238

Qy 241 APSYGVVERVGGDMFVSPKGDATFMKWTCHDMSDBECHLKLKCYEALP 300
 Db 239 APSYGVVERVGGDMFVSPKGDATFMKWTCHDMSDBECHLKLKCYDLP 298

Qy 301 ILPVARDASILPTKAVHIDIMLAINPGGKERTERKEFALKAGAFREGFGRVVAQNTW 360
 Db 299 ILPVARDASILPTKAVHIDIMLAINPGGKERTERKEFALKAGAFQGEVNC-CAENTH 357

Qy 361 IIEFLKK 367
 Db 358 VIEFRKK 364

RESULT 5
 US-09-500-569-4

; Sequence 4, Application US/09500569
 ; Patent No. 6329304
 ; GENERAL INFORMATION:
 ; APPLICANT: Canoan, Rebecca B.
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Shen, Jenny
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase

FILE REFERENCE: BB1327 US NA
 CURRENT APPLICATION NUMBER: US/09/500,569
 CURRENT FILING DATE: 2000-02-09
 EARLIER APPLICATION NUMBER: 60/119,587
 EARLIER FILING DATE: 1999-February-10
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Microsoft Office 97
 SEQ ID NO: 4
 LENGTH: 365
 TYPE: PRT
 ORGANISM: Glycine max
 US-09-500-569-4

Query Match 81.8%; Score 1566.5; DB 2; Length 365;
 Best Local Similarity 80.2%; Pred. No. 1.3e-165;
 Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSTSTKMSSEAAAEEAFVPAKQLTSAVPLVLSAIEVLETEAKAGPAHTS 60
 1 MGSTGETQITPHT--VSDEEANLAFAMQLASAVPLMILKSALEDDLEIETAKAGPGVHLS 58

QY 61 TSDIAKSLPTKPNDAVMDMLRLLASYSUTSLURTDGKIERLYGLAPCKFLRN 120
 59 PTDISQIQLPTONPAPWMDLIRLILACNTLSFSLRTDGGKVERLYGLAPVAKYLVN 118
 Db 121 DDGVSTAALSLMNQDKLUMESWYHTEAVLEGGIPENPKAVGMATEFYHGDPRFTVFN 180
 119 EDGVSTAALSLMNQDKLUMESWYHTEAVLEGGIPENPKAVGMATEFYHGDPRFTVFN 178

QY 181 GMSNHSTITMKKILLETYKGFRGIGSIVDVGGGTGAHNLMTAKYPMIGNIFDLPVTE 240
 179 GMADHSTITMKKILLETYKGFRGIGSIVDVGGGTGAHNLMTAKYPMIGNIFDLPVTE 238

QY 241 APSYRGEVHGGDMFVSVRKGDAIFMKWICHDDWSDEHCKLKCFLKCYEALP 300
 239 APSYRGEVHGGDMFASVPKDAIFMKWICHDDWSDEHCKLKCFLKCYEALP 298

Db 301 ILPVADASLPTKAVHITVIMLAHNPGCKTEREKEFAALKAGGAGFEGR 360
 299 ILPVADASLPTKAVHITVIMLAHNPGCKTEREKEFAALKAGGAGFEGR 357

QY 361 IIEFLKKI 368
 Db 358 IMEFLKKI 365

RESULT 6
 US-09-971-823B-4

; Sequence 4, Application US/09971823B
 ; GENERAL INFORMATION:
 ; Patent No. 6610521
 ; APPLICANT: Cahoon, Rebecca E.
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
 ; FILE REFERENCE: BB1327 US NA
 ; CURRENT APPLICATION NUMBER: US/09/971,823B
 ; CURRENT FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/119,587
 ; PRIOR FILING DATE: 1999-02-10
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO: 4
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-09-971-823B-4

Query Match 81.8%; Score 1566.5; DB 2; Length 365;
 Best Local Similarity 80.2%; Pred. No. 1.3e-165;
 Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSTSTKMSSEAAAEEAFVPAKQLTSAVPLVLSAIEVLETEAKAGPAHTS 60
 1 MGSTGETQITPHT--VSDEEANLAFAMQLASAVPLMILKSALEDDLEIETAKAGPGVHLS 58

QY 61 TSDIAKSLPTKPNDAVMDMLRLLASYSUTSLURTDGKIERLYGLAPCKFLRN 120
 59 PTDISQIQLPTONPAPWMDLIRLILACNTLSFSLRTDGGKVERLYGLAPVAKYLVN 118
 Db 121 DDGVSTAALSLMNQDKLUMESWYHTEAVLEGGIPENPKAVGMATEFYHGDPRFTVFN 180
 119 EDGVSTAALSLMNQDKLUMESWYHTEAVLEGGIPENPKAVGMATEFYHGDPRFTVFN 178

QY 181 GMSNHSTITMKKILLETYKGFRGIGSIVDVGGGTGAHNLMTAKYPMIGNIFDLPVTE 240
 179 GMADHSTITMKKILLETYKGFRGIGSIVDVGGGTGAHNLMTAKYPMIGNIFDLPVTE 238

QY 241 APSYRGEVHGGDMFVSVRKGDAIFMKWICHDDWSDEHCKLKCFLKCYEALP 300
 239 APSYRGEVHGGDMFASVPKDAIFMKWICHDDWSDEHCKLKCFLKCYEALP 298

Db 301 ILPVADASLPTKAVHITVIMLAHNPGCKTEREKEFAALKAGGAGFEGR 360
 299 ILPVADASLPTKAVHITVIMLAHNPGCKTEREKEFAALKAGGAGFEGR 357

QY 361 IIEFLKKI 368
 Db 358 IMEFLKKI 365

RESULT 7
 US-09-204-288-5
 ; Sequence 5, Application US/08204288
 ; Patent No. 5959178
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN DOORSELARE, Jan
 ; APPLICANT: FRITIG, Bernard J.M.
 ; APPLICANT: INZE, Dirk G.
 ; APPLICANT: JOUANIN, Lise
 ; APPLICANT: KNIGHT, Mary E.
 ; APPLICANT: VAN MONTAGU, Marc
 ; APPLICANT: LEGRAND, Michel
 ; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
 ; TITLE OF INVENTION: PLANTS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/204,288
 ; FILING DATE: 10-MAR-1994
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9119279.9
 ; FILING DATE: 10-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB92/01460
 ; FILING DATE: 03-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, Raul N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE DOCKET NUMBER: 206860/SBB36543/UST
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:

Query Match 78.3%; Score 1499.5; DB 1; Length 364;
 Best Local Similarity 77.8%; Pred. No. 3.9e-158;
 Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

MOLECULE TYPE: protein
 US-09-204-288-5

Qy 1 MGSTSETKMSPEAAAEAEAVFVAMQLTSAVLPVNLKSAIEVDLVEFLMAKAGPGAHIS 60
 1 MGSTSEBSQ - SNSLHTTEDAEFLPAMQLSASVLPVNLKSAIEVDLVEFLMAKAGPGAHIS 58

Qy 61 TSDIASKLPLTPKNDPAVMDMLRLIASVLTCSLRTLPDKTIERLYGLAPVCKFLTRN 120
 59 PSELAAQSTONPEAVVMDMLRLIASVLTCSLRTLPDKTIERLYGLAPVCKFLTRN 118

Qy 121 DDGVSIAAISLMMNODKVMSWYHILTEAVLEGGIPPNKAYGMAFEYHGT 180
 119 ADGVSVAPLLMNQDKVLMESWYHLKDAVLDGGIPPNKAYGMAFEYHGTDPRENKVNR 178

Qy 181 GMSNHSITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 240
 179 GMSDHSTMSMKITLEDYKGEGLNSIVDVGSGTGAUTNMVSKVYSIKGNFDLPHVGD 238

Qy 241 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 300
 239 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 298

Db 299 ILPVAAPDTSLATKNTVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Qy 301 ILPVAAPDTSLATKNTVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Db 299 ILPVAAPDTSLATKGVVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Qy 360 W 360

Db 359 W 359

RESULT 8

US-09-500-569-18

; Sequence 18, Application US/09500569

; Patent No. 6329204

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Rafalski, Antoni

; APPLICANT: Shan, Jenie

; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase

; FILE REFERENCE: BB1327 US NA

; CURRENT APPLICATION NUMBER: US/09/971,823B

; CURRENT FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: 60/119,587

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 18

; LENGTH: 358

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: NAME/KEY: UNSURE

; LOCATION: (134)

; OTHER INFORMATION: xaa = ANY AMINO ACID

US-09-971-823B-18

Query Match 77.9%; Score 1492; DB 2; Length 358
 Best Local Similarity 78.1%; Pred. No. 2.6e-157;
 Matches 282; Conservative 39; Mismatches 36; Indels 3;

Qy 1 MGSTSETKMSPEAAAEAEAVFVAMQLTSAVLPVNLKSAIEVDLVEFL 60
 1 MGSTGETQITPHT - VSDEBANFLPAMQLSASVLPVNLKSAIEVDLVEFL 58

Qy 61 TSDIASKLPLTPKNDPAVMDMLRLIASVLTCSLRTLPDKTIERLYGL 120
 59 PSDIASRUPHNPDAVMDMLRLIASVLTCSLRTLPDKTIERLYGL 118

Db 119 EDGVSVAPLLMNQDKVLMESWYHLKDAVLDGGIPPNKAYGMAFEYHGT 178

Qy 181 GMSNHSITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 240
 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Db 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Qy 181 GMSNHSITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 240
 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Db 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Qy 241 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 300
 239 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 298

Db 299 ILPVAAPDTSLATKGVVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Qy 301 ILPVAAPDTSLATKNTVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Db 299 ILPVAAPDTSLATKGVVHVDIVMLAINPGGKERTKEFEALAKGAGTGFARLVALTGS 358

Qy 360 W 360

Db 358 Y 358

RESULT 9

US-09-971-823B-18

; Sequence 18, Application US/09971823B

; Patent No. 6610521

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase

; FILE REFERENCE: BB1327 US NA

; CURRENT APPLICATION NUMBER: US/09/971,823B

; CURRENT FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: 60/119,587

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 18

; LENGTH: 358

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: NAME/KEY: UNSURE

; LOCATION: (134)

; OTHER INFORMATION: xaa = ANY AMINO ACID

US-09-971-823B-18

Query Match 77.9%; Score 1492; DB 2; Length 358
 Best Local Similarity 78.1%; Pred. No. 2.6e-157;
 Matches 282; Conservative 39; Mismatches 36; Indels 3;

Qy 1 MGSTSETKMSPEAAAEAEAVFVAMQLTSAVLPVNLKSAIEVDLVEFL 60
 1 MGSTGETQITPHT - VSDEBANFLPAMQLSASVLPVNLKSAIEVDLVEFL 58

Qy 61 TSDIASKLPLTPKNDPAVMDMLRLIASVLTCSLRTLPDKTIERLYGL 120
 59 PSDIASRUPHNPDAVMDMLRLIASVLTCSLRTLPDKTIERLYGL 118

Db 119 EDGVSVAPLLMNQDKVLMESWYHLKDAVLDGGIPPNKAYGMAFEYHGT 178

Qy 181 GMSNHSITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 240
 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Db 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Qy 181 GMSNHSITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 240
 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Db 179 GMADHSTITMKKILETYKFRGLGSVUDVGGTGAHNMIAKPMIKG 238

Qy 241 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 300
 239 APSYGVVERHVGDDMFVSVPKDAIFMKWICHWDSDBHCFLKPLKCYEALP 298

RESULT 10
 US-09-500-569-6
 ; Sequence 6, Application US/09500569
 ; Patent No. 6329204
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; APPLICANT: Rafalski, Antoni
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
 ; FILE REFERENCE: BB1327 US NA
 ; CURRENT APPLICATION NUMBER: US/09/500,569
 ; CURRENT FILING DATE: 2000-02-09
 ; EARLIER APPLICATION NUMBER: 60/119,587
 ; EARLIER FILING DATE: 1999-February-10
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 6
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 ; US-09-971-823B-6

Query Match 65.0%; Score 1244; DB 2; Length 356
 Best Local Similarity 65.1%; Pred. No. 1.1e-129;
 Matches 239; Conservative 50; Mismatches 66; Indels 5;
 Qy 1 MGSTSETKMSPEAAAEERAFVAFAMOLTSASVLPVNLKSAILEDVLEIMP
 Db 1 MGST---ADMASADAEACMTAQLQVYV
 Qy 61 TSDIASKLPTKNPDAAVMDRMLRLLASVSVLTSRSLTLPDKTERLYGI
 Db 55 PAEVAKLPSFTANPAADMDRMLRLLAAYNVSTCMEBGKDRGSLRSRYG
 Qy 120 NDDGYSIAASLIMQDKVLMESWTHLTTEAVLLEGSIPEKNAYGMAFEYIG
 Db 115 NEDGVSMAALALMNDKVLMESWYKLDVLDGGIPFNKAYGMSAFAEYIG
 Qy 180 NGMSNHSTITMKKLETYKCFEGGSWVUGGTGAHNMILAKYPMIKG
 Db 180 NGMSNHSTITMKKLETYKCFEGGSWVUGGTGAHNMILAKYPMIKG
 Qy 1 MGST---ADMAASADEEACMTAQLQVYV
 Db 61 TSDIASKLPTKNPDAAVMDRMLRLLASVSVLTSRSLTLPDKTERLYGI
 Qy 55 PAEVAKLPSFTANPAADMDRMLRLLAAYNVSTCMEBGKDRGSLRSRYG
 Db 114 PAEVAKLPSFTANPAADMDRMLRLLAAYNVSTCMEBGKDRGSLRSRYG
 Qy 120 NDDGVSIAASLIMQDKVLMESWTHLTTEAVLLEGSIPEKNAYGMAFEYIG
 Db 115 NEDGVSMAALALMNDKVLMESWYKLDVLDGGIPFNKAYGMSAFAEYIG
 Qy 180 NGMSNHSTITMKKLETYKCFEGGSWVUGGTGAHNMILAKYPMIKG
 Db 180 NGMSNHSTITMKKLETYKCFEGGSWVUGGTGAHNMILAKYPMIKG
 Qy 1 MGST---ADMAASADEEACMTAQLQVYV
 Db 231 BAPPPGVTFVGGDFQKQPSGDAILKMWILHDWSDEHATLKNCYDAl
 Qy 300 CILPVADASLPTKAVVHIDVIMLAHNPGCKERTKEFEALAKGAGFEGE
 Db 291 CILPVNPETATPKAQGVFHDMIMLAHNPGCREREREFERALAKGAGFKAT
 Qy 360 WIEFLK 366
 Db 350 FAIEFTK 356

RESULT 11
 US-09-971-823B-6
 ; Sequence 6, Application US/09971823B
 ; Patent No. 6610521
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
 ; FILE REFERENCE: BB1327 US NA
 ; CURRENT APPLICATION NUMBER: US/09/500,569

Query Match 56.0%; Score 1073; DB 2; Length 362
 Best Local Similarity 55.0%; Pred. No. 1.3e-110;
 Matches 206; Conservative 66; Mismatches 88; Indels 3;
 Qy 1 MGSTSETKMSPEAAAEERAFVAFAMOLTSASVLPVNLKSAILEDVLEIMP
 Db 1 MGSTAVEKVA---VATGDBEACMYAVKLAASILPMLTKNAIELGMELIN [S 60
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 ; US-09-500-569-14

RESULT 12
 US-09-500-569-14
 ; Sequence 14, Application US/09500569
 ; Patent No. 6329204
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; APPLICANT: Rafalski, Antoni
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase 1
 ; FILE REFERENCE: BB1327 US NA
 ; CURRENT APPLICATION NUMBER: US/09/500,569
 ; CURRENT FILING DATE: 2000-02-09
 ; EARLIER APPLICATION NUMBER: 60/119,587
 ; EARLIER FILING DATE: 1999-February-10
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 14
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 ; US-09-500-569-14

Qy 61 TSDIASLKPLTK-NPDAVMLDRMLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTR 119
 Db 57 PSBRAAQOLPSKANPRAEVMDRMLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTR 115

Qy 120 NDDGUSIAASLMLNQDKVLMESWAHTEAVLEGIPPNKAYGMAFBYHGDPRENTVEN 179
 Db 117 NEDGASMAGLMLMTDKVMSWVYKDVALLEGIPPNKAYGMAFBYHGDPRENTVEN 175

Qy 180 NGMNSHSTITWKKLKBTYKCPREGLEGSSWVDGGTGAHNMITAKCPWMKGINFDPHIVIE 239
 Db 177 BAMLNHSITITKKLKBTYKCPREGLEGSSWVDGGTGAHNMITAKCPWMKGINFDPHIVIE 236

Qy 240 EAPSYPGVENGGDMFVSPKGAFPMWKWCHDWSDEHCKLKKCYEALPTNGVILAE 299
 Db 237 EAPYPGVQHAGDMFKCKVSGDALLKKLKWLNWTDDYCMTRNLYDALPMNGKVVIE 295

Qy 300 CILPVADSLPTKAVHIDVIMLAMNPGKERTKEFELAKAGAGFEGFRVVAACANT 359
 Db 297 GILPVKPDAMPSTQMFQDVMMLHUTAGGERELSEFESLAKAGFS--TVKTSYIYST 354

Qy 360 -WIEFLK 366
 Db 355 AWIEFLK 362

RESULT 13
 US-09-971-823B-14
 ; Sequence 14, Application US/09971823B
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
 ; FILE REFERENCE: BB1327 US NA
 ; CURRENT APPLICATION NUMBER: US/09/971,823B
 ; CURRENT FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/119,587
 ; PRIOR FILING DATE: 1999-02-10
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO: 14
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: *Triticum aestivum*
 ; US-09-971-823B-14

Query Match 56.0%; Score 1073; DB 2; Length 362;
 Best Local Similarity 56.0%; Pred. No. 1.3e-110; Mismatches 88; Indels 8; Gaps 5;

Matches 206; Conservative 66; Mismatches 88; Indels 8; Gaps 5;

Qy 1 MGSISETKMSPEAAAEAFVAMQTSASVLPVNLSAIEVDLLEIMAKAGPAGHIS 60
 Db 1 MGSTAVEKVA---VATGDEEACMVAKLAASILPNTKNAIEGLMLETIPLV 56

Qy 61 TSDIASLKPLTK-NPDAVMLDRMLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTR 119
 Db 57 PSEVAQOLPSKANPRAEVMDRMLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTR 116

Qy 120 NDDGUSIAASLMLNQDKVLMESWAHTEAVLEGIPPNKAYGMAFBYHGDPRENTVEN 179
 Db 117 NEDGASMAGLMLMTDKVMSWVYKDVALLEGIPPNKAYGMAFBYHGDPRENTVEN 176

Qy 180 NGMNSHSTITWKKLKBTYKCPREGLEGSSWVDGGTGAHNMITAKCPWMKGINFDPHIVIE 239
 Db 177 BAMLNHSITITKKLKBTYKCPREGLEGSSWVDGGTGAHNMITAKCPWMKGINFDPHIVIE 236

Qy 240 EAPSYPGVENGGDMFVSPKGAFPMWKWCHDWSDEHCKLKKCYEALPTNGVILAE 299
 Db 237 EAPYPGVQHAGDMFKCKVSGDALLKKLKWLNWTDDYCMTRNLYDALPMNGKVVIE 295

Qy 300 CILPVADSLPTKAVHIDVIMLAMNPGKERTKEFELAKAGAGFEGFRVVAACANT 359
 Db 297 GILPVKPDAMPSTQMFQDVMMLHUTAGGERELSEFESLAKAGFS--TVKTSYIYST 354

Qy 360 -WIEFLK 366
 Db 355 AWIEFLK 362

RESULT 14
 US-08-186-833-4
 ; Sequence 4, Application US/08186833
 ; GENERAL INFORMATION:
 ; APPLICANT: Tarczynski, Mitchell C.
 ; APPLICANT: Jensen, Richard G.
 ; TITLE OF INVENTION: Transgenic Plants with Enhanced Mannit Correspondence Address:
 ; ADDRESS: Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53701-2113
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word, Version #5.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,833
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/1871,416
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 2786
 ; REFERENCE/DOCKET NUMBER: 9221490026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 251-5000
 ; TELEFAX: (608) 251-9166
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 365 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-186-833-4

Query Match 54.7%; Score 1047; DB 1; Length 365
 Best Local Similarity 54.3%; Pred. No. 1.1e-107; Mismatches 88; Indels 8; Gaps 2;

Matches 190; Conservative 70; Mismatches 88; Indels 8; Gaps 2;

Qy 18 EEEAFVFMQTSASVLPVNLSAIEVDLLEIMAKAGPAGHISSTDIAK
 Db 18 DEQLAGLAVTIANAAFPMLKSAIEKLDIFSKAGCGVFVSIASQ
 Qy 78 MLDMLRLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTRNDGVSIA
 Db 78 LDMLRLRLASVSYLTSCLRUDPKIERLYGLAPVCKFLTRNDGVSIA
 Qy 198 KGFEGISGVTDGGTGAHNMITAKCPWMKGINFDPHIVIEAPSYGV
 Db 197 NGFDNPKVJUDVGENIGVNMIVAKTHIGKINYDPLPHIVIAPSYGV
 Db 137 MMESWPHLNUYDLEGGVPPKRAHGMQFDYTGTDERFHVENDMAHHT
 Qy 199 KGFEGISGVTDGGTGAHNMITAKCPWMKGINFDPHIVIEAPSYGV
 Db 197 NGFDNPKVJUDVGENIGVNMIVAKTHIGKINYDPLPHIVIAPSYGV
 Db 258 VPKGDAIFMKWICHDSDEHCKLKKCYEALPTNGVILAECLPVAD
 Qy 257 IPQADAIFMKWWLHDWSDEHCKVNLINKCYESLAKGKIIIVESLIPVIE

RESULT 15
 US-08-204-288-7
 ; Sequence 7, Application US/08204288
 ; Patent No. 5959178
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN DOORSELARE, Jan
 ; APPLICANT: FRITIG, Bernard J.M.
 ; APPLICANT: IMZE, Dirk G.
 ; APPLICANT: GOUANTIN, Lise
 ; APPLICANT: KNIGHT, Mary E.
 ; APPLICANT: VAN MONTAGU, Marc
 ; APPLICANT: LAGRAND, Michel
 TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
 TITLE OF INVENTION: PLANTS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESS: CUSHMAN DARBY & CUSHMAN, L.L.P.
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D. C.
 COUNTRY: U.S.A.
 ZIP: 20005-3518
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/204,288
 FILING DATE: 10-MAR-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9119279.9
 FILING DATE: 10-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/01460
 FILING DATE: 09-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, Paul N.
 REGISTRATION NUMBER: 16,773
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-204-288-7

Query Match 54.6%; Score 1045.5; DB 1; Length 365;
 Best Local Similarity 57.1%; Pred. No. 1.6e-107; Matches 210; Conservative 51; Mismatches 96; Indels 11; Gaps 7;

QY 318 IDVIMLAHNPGGKERTKEFEALAKGAGFEGFPRVVASCAVNTWIEFLKK 367
 Db 317 LDCHTLVHNOGGERSKEDFEALASKTGFSVTDVIC-CAYDTWWMELYKK 365

Db 119 DEDGASMGPLLAIQDKVIFINSWFLKORAVLEGCGVPFDRVGHVHAFESPY 178
 QY 179 NNGMSNHSTITMKKILETYKGFFCIGLSVUDVGGTGAHNMILAKYPMK 238
 Db 179 NKAMINHTTVMKCKLLENKGFFNLKTDVGGGLVNMKLMITK 238

Db 239 EADSYPGVHEVGDMFNSVPKGDAIFMKWICHDSDEBOLKFLKKCBEAJ 298
 QY 239 QHAFSYPGVHEVGDMFNSVPKGDAIFMKWILADWSHNLKJNKCYKAJ 298

Db 299 ECTLPVAPPASLPLPKAVVIIIDVIMLAHNPGGKERTKEFEALAKGAGFEGI 358
 QY 299 EATLPVKPDDITAVVGVSQCDLIMAQNPGKERSBEEFRALATEAGFKQ 358

Db 359 TWIEFLK 366
 Db 358 PWMEFCK 365

Search completed: December 12, 2005, 08:48:28
 Job time : 48 SECs